

FIGURE 1

CGGACGCGTGGGTCCGAGGCCAAGGTGACCGGGGACCGAGCATTCAAGATCTCGTCGGTAGA
 CCTGGTGCACCAACCAC**A**TGCTGGCTGCAAGGCTGGTGTCTCCGGACACTACCTCTAGG
 GTTTCCACCCAGCTTCACCAAGGCCTCCCTGGTAAGAAATTCCATCAGAAGAACATCA
 ATGGCTGTTAACACCTAGCAGGGAAATATGCCACAAAACAAGAATTGGGATCGGCGTGAAA
 GAACTGGCCAAGAACCTCAAAGAGGCAGCATGGAACCATCGATGGAAAAAAATATTAAATT
 GATCAGATGGGAAGATGGTTGTTCTGGAGGGCTGCTGGTGTCTGGAGCATTGTCATA
 CTATGGCTTGGGACTGCTAATGAGATTGGACTTGAAGGGCTGTAAATTGGCCTCAGT
 ATGTCAGGATAGAACATTCCACCTATGACTACCTAGCAGGAGTATTGGTTAACAGCT
 TTGCTGCCATAGCAACAGCCTGTTCTCATGAACTCATGATGAGAGGCTTGG
 GGTGACAATTGGTGTGACCTTGCAGCCATGGTGGAGCTGGAAATGCTGGTACGATCAATAC
 CATATGACCAAGAGGCCAACAGCATTGCTTGGTGTACATTCTGGTGTATGGGT
 GCAGTGGTGGCTCTCTGACAATATTAGGGGCTCTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGGGAGGCCCTCCACTCTGGCCATGTGCCCCCAGTGAAAAGTTCTGA
 ACATGGGTGACCCCTGGGAGTGCCCTGGGCTCGTCTTGTGTCTCATGGGATCTATG
 TTTCTCCACCTCACCCGTGGCTGGCACTCTTACTGGCAATGACGGTGGATT
 AGTCTTTCTGAGCATGTTCTCTGATGACCCAGAAAGTATCAAGCTGCAGAAGTAT
 CACCAATGTGAGGTTCAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAA**TG**
AAGTGA
 CTGCTTCTGGCTTCTCTGTCACATCAAAATATCTGTTAACAGGATGATATGC
 ATTAATATGTTGACAGCAGCTTCTGTAAGTTAGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCCTCAGGTCTGCCTTTTTCTGGAGAAATAAATGCA
 GATATCCCTCCAAATAAGCACACACATTTCATGTTGAGTGTGAGTATTAAATGTT
 TTGGTGAATGTAAGAAACTAAAGTTGTTGTCATGAGAATGTAAGCTTTTCTACTTTAAA
 TTTAGTAGGTTCACTGAGTAACATAAAATTAGCAAACCTGTGTTGCATATTGGAGT
 GCAGAAATATTGTAATTAAATGTCATAAGTGATTGGAGCTTGGTAAGGGACAGAGAGAAG
 GAGTCACCTGCAGTCTTTGTTTTAAATACTAGAACTTAGCAGTGTGTTATTGATTA
 GTGAGGAGGCCAGTAAGAAACATCTGGTATTGGAAACAAAGTGGTCAATTGTTACATT
 GCTGAACCTAACAAAATGTTCATCCTGAACACAGGCACAGGTGATGCATTCTCCTGTTG
 CTTCTCAGTGCTCTTTCAATATAGATGTTGACTTGACAGAATGTTAATC
 ATACAGAGAATCCTGATGGAAATTATATGTTGTTTACTTTGAATGTTACAAAAGGAA
 ATAACCTAAAATATTCTCAAGAGAAAATTCAAAGCATGAAATATGTTGTTCCAG
 AATACAAACAGTATCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLTPSREYATKTRIGIRRRTGQEIK
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSIAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTI LGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPI
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGLVLFSMFLLYDTQKVVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCCTGCCCGTGGTCGAATTGGTGGCGCACGTCGCCGTCTCCGCCCTCTGCAT
 CGCGGCCCTCGGCGGCTTCCACCTAGACACCTAACAGTCGGGAGCCGGCGCTCGTGAGGG
 GGTGCGGACGGGGAGTCGGGCGGTCTTGTCGATCTTGGCTACCTGTGGGTCGAAG**ATG**TGG
 ACATCGGAGACTGGTTAGGAGCATCCCGGATCAGCGCTATTGGTTCGCCACCGTC
 GCCGTGCCCTGGTGGCGCAAACCTCGGCCATCAGCCGCCAACCGTC
 AGCCTTCTTATCGCTTCAGATTGGAGGCCAATCACTGCCACCTTTATTCCCTGTGG
 GTCCAGGAACCTGGATTCTTATTGGTCAATTATATTCTTATTCAGTATTCTACGCCA
 CTTGAAACAGGAGCTTGTGGAGGCCAGCAGACTATTATTCATGCTCTCTTAACTG
 GATTGCGATCGTGATACTGGCTTAGCAATGGATTCAGGTTGCTGATGATTCTCTGATCA
 TGTCACTTATGCTGGGCCAGCTGAACAGAGACATGATTGATTCATTGGTTGG
 ACACGATTAAAGGCGTCTATTACCTGGGTATCTGGATCAACTATATCATGGAGG
 CTCGGTAATCAATGACCTTGGGAAATCTGGTGGACATCTTATTTCTAATTC
 GATACCAATGGACTTGGAGGAGAAAATTCTATCCAACCTCGATTGGTACCCCTGG
 CTGCCAGTGGAGGAGGAGTATCAGGATTGGTGTGGCCCTGCTAGCATGAGGGAGC
 TGCTGATCGAAATGGCGAGGGGGAGACAACCTGGGGCAGGGCTTCGACTGGAGACC
 AG**TGA**AGGGCGGCCCTGGCAGCCCTCAAGCCACATTCCCTCCAGTGTGGTG
 CACTAACACTGGCTCTGGCTAACACTGTGGACCTGGACCAACTGATGATGCTTC
 AGTACGAGAACAAATTCTTAACTCCGAAGAAAATATAAGTGTCCAAAGGTTACGAT
 TCTCATCAAGTCTTACTGCTGAGAAGAACAAATCTTAACTGTCGAAATTGCAAAACTGAC
 TACATTTTGGTGTCTCTCTCCCTTCCGGCTGATGAAATAATGGGTTTAGGGCTCT
 AATCTGCTGGCATTGAGCTGGGGCTGGTCAACCAACCCCTTAAAGGACCTTATCT
 TCTTCGACACATGGCTCTCTCCACCTTTCCCACACATTGCAACTAGAAAATG
 CCCATAAAATGGCTCTGCCCTGACAGGTTCTGTATTATTGACTTTGCCAAGGCTGGT
 ACAACAACTATCACTGGTATTCTCCCTTTGGTGGCAGAACACTGTTACATAGGGGAG
 AAGACAGCACCGATGAAGCGTTCTCAGGTTGGGAACTGCTGACTGACATCGTTG
 AACCGTTGGCACTCTCAGGATATTAAAAAAAGTACCAACTGAGITCACTGAGGCCA
 CAGATTGGTATTAAAGATGAGATCAGGGTTGGTGTGGACTGAGTTGGGTTAGTGA
 TCAAGACTGATGGAGTGGCACTAACATGGGTAGGTTAAACCATGGGGATGACCCCC
 TTTGGTTTCATATGATGGCTCTGGCTTGTGAGCTGGAGTAGTTGGTTGGCTTGT
 TAGGAGGATCCAGATCATGGTGGCTACAGGGAGATGCTCTTGTAGAGGTTGGGATTG
 ATTCCCAATTCACTCATCTGGGATATGGTCTCATGGTCAATTGAGTATTAACTT
 CGCTATTAAATGTCATTTTGCCTATCCCGCTTTGGTCTATGGTCAATTAACTT
 GAGGAAGGCCAGCTCTCTGCACTGAGTACATTTAAAGCTTAAAGCTAATGTAAG
 AGGAAATAACATGATTAAAGGTGAAATGGCTTAAAGCTTAAAGCTTAAAGGTTGG
 TTTTGAGTCATGAATTACAAGCTGTGAATCAGACCCAGCTTAAATACCCACCTTT
 TCGTAGGTGGCTTCTCATGAGCTGGCTCATACCAAAATAAGGTTGGGTTAGG
 TGGCTTTCACACAGTTTTATTATGACGTATCTGAAAGCAGACTGTAGGAGCAGT
 ATTGAGTGGCTCACTGGGCAACTAAAAGGCTTCAACAGTTGGTGTGATGTTCT
 TTCAGGAAACATTGTCGCTCAACTGATGACTATTCTTCCCACTCTTAAACAGTGT
 GTGTGTATCTTGGGCTCATGAGACTGGCAACAAACTTAAAGTTACTTGTAA
 TACTTCTCCATATTAAATTATGATAAAATAGGTGGGAGACTGCTGAACCTTA
 ACTGTCATGTTGAGTGGGAGACTTGTGAAATGAGTTGGGAGACTTGTGATG
 CCAATTATGTCGACGTCACACTCATGTCAGGGCTGGAGACTCATGTCATG
 TTTCTGACAGTGAGTGACCCGGAGACTCTCTGGTGTACCCATTACAGTCAG
 CAGTCATTTCCTTAAGGTTAACAGTATTAGAAGCTTCACTGTTGACCT
 ATGAAGTTATTCTCTTAAACATGGTAGGAGCTGATGACGTTATTGATTTGT
 ATGTTCTGGAATAATTACCAAAACAGCTATTGAGTTGACTTGACAAAGGCCAA
 TGACAGTGGATTCTTACAAATGAAAGGGGGAAATCTTATTGATAAGGACTTCC
 TTTTGTAACATGTTTATTGGTAAATTGTAATTAAAGTGTGAACTT

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVVAQLNRDMIVSFWFGRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

009252144111

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTCGATTAACGGTTG
 GTAGCTTCTATCCTGGGGCTGAGCAGTGCAGCTCTCCCTACTCCCTCGGCT
 CCTTGCGCCAAAGGCTAACCGGGTCCGGCGGTCTGGCCTAGGGATCTCCCCGTTGCC
 CCTTGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGTAGTGGAGAGCATCG
 CGGGGTTCTCGAGGCCAGACTGGTCCATCCCCTCTGGACTTGTGGAACAGAAATGT
 GAAGTTAACGTCAAAGGGAGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTATTG
 GGCCTGTGTTCCCTTGTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATT
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTG
 AATGAAGATCAATTCAAGAAGCATGCACTTCTCTTGCAGAACAGCCATACATCACAGGC
 CATTTCGAAACCTGTGTTGGCAGCAGAAGATTTACTATCTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAAGCTGCAAGCCATTGAAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAAACACGAAGAGATGAAAATCCT
 GAGGGAGTTCTAGAAAATCAAAGAGGAATATGACCAGGAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAACAGAAGAGCCACAGTCATTCCAGTGAAGCTGAAATAG
 AATAATTCCAAGGGGATGGTGAACATTGACACCCCACCTCAGAAGTTAAATGCAATT
 TGCTAATCAGTCATAGAACCTTGGGAAGAAAAGTGGAAAGGTCTGAAACTCTCCCTCC
 CACAAAAAGGCCTGAAGATTCCCTGGCTTAGAGCATGCGAGCATGAGGACCAATAGCAAAC
 TTATCAGTACTTGGACAGAAGAACCTCGGCAACGAGAACACTATCTCAAGCAGAAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAATATGGAGCAGAAG
 GAAAACCCACTGGGGAGGTAGAGGAATGACAGAGAAACAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGTTATAATAAG**TA**
ATAATTAAGAACATTAACAAATGGAAGTCAAATTGCTTAAATAATTATTTAGTC
 CTTACACTG

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FIGURE 6

MAAEEEDEVEWVVESIAGFLRGPDWSIPILDVFVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGVLPDCLTDGSDVVSDLEHEEMKILREVL
RKSKEEYDQEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLM
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAAEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAGAACACTGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTCAAGAACGATGCACCTCCCTTGCAGAACGACCCATACATCACAG
GCCATTTTGCAACCTGTGTTGGCAGCAGAAGATTTACTATCTTAAAGCAATGATGGTCC
AGAAAAAACATTGAAATGCAGCTGCAAGCCATTGAAATAATTCAAGAGAGAAATGGTGTATTA
CTGACTGCTAACCGATGGCTCTGATGTGGTCAAGTGACCTTGAACACGAAGAGATGAAAAT
CTGAGGGAAGTTCTAGAAAATCAAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTGTCTGCAATAGCGGCTTAGAGGGAGGGCTTTCGCCTATACCTACTG
 TAGCTCTCACGTATGGACCCTAAAGGCTACTGCTGACTACGGGGTAGACAGTTACTG
 TCTCAGCCTAGGATGTGCCTCTCCACTAGAACGCTCTCTGAGGGAGGTAATTAAAAAC
 AGTGGAA**ATG**AAAAAACAGTGCTGTAGTCATCTGTAAATATGCTCTTGTCAACAATGTATAC
 ATTCTGCTAGGTGCCATTCTGCTTAAGCTCAAGTCGCATCTACTAGTGAAGTATT
 CTGCCATAGAAGAAAACAAGTATGATTATCTCCAACACTACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTCTGTCCTGTCTGTATAAAGAAAGATCATCAAAGTAG
 AAATTGAAATATGCTCTGGAGGAATTCTGATGATTCTGAAGTGGTCATTCTGCT
 TTCTTATTCTCTGGATAACTTGATGTCTCTATGTCCTGTCTATCTCAACCAGCCATG
 GCTGTTATCTCTCAATTAGTCAGTATAACACAGCTCTCTGACTTCAGGATAGTGTGAA
 GAGGCGCTAAACTGGATCAGTGGCTCTCTGACTTTGTCATTTGTCTATGGCCCT
 TGACTGCCGGATAAACTTACAGACAATTGGCAGGAGCTGGATTATCACAGTC
 TTTTCAGCCTTCAATTCTGCCCTTTCAGAAGTGAGTGCCCAGAAAAGACAATTG
 TACAGCAAAGGAATGACTTCTGAGCTAAATGGAACACACAGCAGAGTTTCTGCT
 ACATCCGCTTGGCATGGGCCATGTTCTTATTAGTCAGTGTGTTTATTCTCAATGGT
 AATATCTATAATGAAAGATACTGAAGGAGGGAAACAGCTCACTGAAAGCATCTCATA
 GAAACAGCAAACCTATTTCTTGCATTCTGTTAATGGGCTGACTCTGGGCCCTCAGAGGA
 GTAACCGTGTAGCATGAGTAAAGACTGGGATTTTGGCCACAGTCGATTTCAGGCC
 CTTATTGTAACTGATTCCAGGGCTTCTCAGTGGCTTCTATTGCAAGTTCTGGATAA
 CATGTTCCATGTCGATGGCCAGGTTACACTGTCATTATCACAAACAGTGTCTGCTGG
 TCTTGAACCTCAGGGCTCTCTGGAAACGGCCATCAGTCCTCTCTCTATA
 TTATTATAATGCCAGAACGCTCAAGTCCGAAATACGCACCTAGGCAAGAAAGGATCG
 AGATCTAACTGGCAATCTGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAACCCAAGAGTGTAGTCAGATGAAGATACTTC**TAAC**TGGTACCCACATAGTTGCA
 GCTCTGCAACCTTATTTTCACATTTCAGTTGTAATTTATCTTCACTTGTATA
 AACCGAAAATGTTCTAAATCTTCAATTCTGTCATATCTAGTACTCTTAAATGGT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTCTAAAGAACTGATAACAGGAGTAACA
 ATATGAGAAGATTCATTAATCTCACTGACTTGTAAATCTAGAAGTTATATGTCGACATTAT
 TTCTGGCTTCAAGCTTCAAAAACCTGTAATATCTGTTAGCTATAGCTGTATAT
 ACACATAGAGATCAATTGCCAATATTCAACATCATGTTAGTTAGTTACATGCCAAGT
 CTTCCTTTTAACATTTAAAGCTAGGTTGTCCTGTAATTGGAGGCCCTAGAGATAGT
 CATTTCGCAACTAAAGAGCACGGGACCTTCTAAAGGCTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTTGGGATGATGTTGCTGTAATATTGCTGAAGAAGCAGT
 TTCTCAGACACACATCTCAGAATTAAATTGAGAATTCTAGGGAAATTGGATTTTGT
 AATAATCTTGTGTTAACATGGTCTCTAGTCACCTAGTACCTGTTACACTGTATTAA
 AGTCATTAAACAAAGGCCAGGGCTTCTCAGTTGAGGAGAAAATCTTGT
 GTCAATTACTCTGAAATTATTACATTGGAGAATTAAGAGGGCATTTATTGTTAGTACT
 AATTCAAGCTGTGACTTGTATATCTTCAAGAGTTGAAATGCTGCTTCAGAATCATAC
 CAGATTGTAGTGAAGCTGCTTAGGAACCTTAAAGGGATCCTTCAAAAGGATCATT
 ACCAAACACATGTTGACTTTAACTGATGTATGAATATTAAACTCTAAAAATGAAAGACC
 AGTAATATAAGTCACCTTACAGTCTACTTCACACTAAAAGTCATGGTATTTTCATG
 GTATTGTCATGCAGCCAGTTAACCTCGTAGATAGAGAAAGTCAGGTGATAGATGATATTAA
 AAATTAGCAACAAAAGTACTGCTGCTCAGGGCTATGCAGCTGGTGTGATGATAAGAGGTGG
 CTTCACGGCAGGCTGTATGTTACAGACTACCATACTGTAATATGAGCTTATGGTGT
 CATTCTCAGAAACTTATACATTCTGCTCTCTCTTAAGTTGATGCAAGATGAATA
 AGGTAATATACTATTATAATTCAATTGATGATTCACACAAATAATGACTGGCAAGAATTG
 GTGGAAATTGTAATTAAATAATTAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQS RNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV
IFSNFSIITTALLFRIVLKRRLNWIQWASLLTFLSIVALTAGTKTLQHNLAGRGFHDAFF
SPSN SCLLFRSECPRKDNC TAK EWTPEAKWNTTARVF SHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESFTIQNSKLYFFGILFNGLLQRSNRDQIKNC GFFYGHSAF SVALI
FVTAFQGLSVA FILKFLDNMFHVILMAQVTTVIITVSVLVFDFRPSLEFFLEAPS VLLSIFTI
YNASKPQVPEYAPRQE RIRDL SGNLWERSSGDGEELRLTPKSDESDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTCCAATCCGGACGTAATCGTGGTTTG
TTCTGCAATAGCGGCTTAGAGGGAGGGCTTTCGCCTAACCTACTGTAGCTCTCCAC
GTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGGTTCTTCACTAGAAGCTTCTGAGGGAGGTAATTAAAAAACAGTGAATGGAA
AAACAGTGTGTAGTCATCCTGTAATATGCTCTGCAACAATGTATACTTCTGCTAGG
TGCCATATTCAATTGCTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCAATTCTGTTATAAAGAAAGATCATCAAAGTAGAAATTGAAATA
TGCTTCTGGAAGGAATTCTGATTTCATGAAGTGGTCCATTCTGCCTTCTTATTCC
TGGATAACTTGATTGTCTTCTATGTCTGTCTATCTCAACCAGCCATGGCTGTTATCTC
TCAAATTTAGCATTATAACAACAGCTTCTATTCAAGGATAGTGCTGAAGAGGGCGTCTAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTGTCTATTGTGGCCTTGAUTGCCGGGA
CTAAAACTTA

FIGURE 11

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGCCGGCTGGCTAGCGCGCGGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCATGCCGGGAGAGCAT
 CCCGTCACCAAGGTCCAAGCGGCCGGCCGGCATGGCCAAGGAGAAAGGCAGCGAG
 AGCGGCTCGCGGGCTGCTACCCACCAGCATCTCCAAGACTGAACGCCGGCCCA
 GGTGAAGAAAAGAACGGAAAAAGAAGAACACAGTGTCTGTTCAACAAAGCTTGATG
 CACTTGGGGAGCCCCCTACCAAGGTGACGGGCTGTGCCCTGGTTCTCCCTCAGATCTAC
 CTATTGG**AATGT**GGCTCAAGGTGGCCCTTCTCTGCCCATCATCTGTGGGCCAGC
 CTGGGATGCCATCACAGACCCCTGGGGCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTGCCCTATGCCCTGGATCATCTCTCACGCCCTGGCCCTATTGCCACTTCTC
 ATCTGGGTCTGCCCCACTTCCCACAGGCCAGACCTATTGGTACCTGCTTTCTATTGCC
 CTTTGAAACAATGGTCAGCTTCCATGTCCCTACTCGGCTCTACCATGGTACAG
 ACCGAGCAGACTGAGGGGATTCTGCCACCCCTATCGGATGACTGTGGAAGTGTGGCAC
 AGTGTGGGACGGGATTCAGGAGCAAATCGTGGCCAAGCAGACACGCCCTGGTCCAGG
 ACTTCATAAGCTCAAGTAGCTTACAAAGTCAGGCCACCATACACATGGCACCAACTAC
 AGGGAAACGCAAAGGCATACCTGTGGCAGGGGATTGTCTGTATCTATAATCT
 TGCTGTATCTGATCTGGGCTGGGGACAGAGAGAACCTATGAAGGCCAGCAGTGTG
 AGCCAATGCCCTACTTCGGGGTACGGCTGGTATGAGCCACGCCCATACATCAAACCTT
 ATTACTGGCTTCCCTTCACCTCTGGCTCATGCTGGTGGAGGGAACTTGTCTGTGTT
 TTGCACTTACACCTTGGGCTTCCGCAATGAAATTCAGAATCTACTCTGGCCATCATGCTCT
 CGGCCACTTAAACCATTCCCATGGCAGTGGTCTTGACCCGGTTGGCAAGAAGACAGCT
 GTATATGTGGGATCTCATCAGCAGTGGCATTTCTATCTGGTGGCCATCTGGAGACTAA
 CCTCATCATTACATATGCGGTAGCTGGCAGTGGCATCAGTGTGGCAGCTCCCTTCTAC
 TACCCGGCTCATGCTGGTATGTCATTGACGACTTCCATCTGAAGCAGCCCATCTCCAT
 GGAACCGAGCCCATCTCTCTCTCTATGTCTCTCACCAGTTGCCCTGGAGTGTCT
 ACTGGGCAATTCTACCCCTCAGTGTGACTTGCAGGGTACCGAGACCCGTGGCTCGCAGC
 CGGAACGTGCAAGTTTACACTGAACATGCTGTGGCAGATGGCTCCCATAGTCTCATCTG
 CTGGGCTGCTGCTCTCAAATGTAACCCATTGATGAGGAGAGGGGGCGGAGAATAAGAA
 GGCCCTGCAAGGCACTGAGGGACGGGCCACAGCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCTC**TAGGGCCCCC**ACGGTGGCCAGGCCACATGCAAGGCCACAG
 AAGGGATCAAGGACCTCTGCCGCTTGTGAGCAGCTGGACTCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCCAAGGACACTTGCCTGTGCTCACTGTGGGGCCGCTGCTG
 TGGCCTCTGCTCCCTCTGCCCTGTGGCTGCCAGGGGCAAGGCCCTGGGCTGCCACTGTGAATA
 TGCCAAAGGACTGATCGGGCTAGCCGGAAACTAATGTAGAAACCTTTTACAGAGCC
 TAATAATAACTTAATGTGTCATAGCAATGTGTGTATGTATGTCTGTGAGCTA
 TTAATGTTATAATTTCATAAAAGCTGGAAAGC

FIGURE 12

MWLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQQQIVGQADTPCFQDFNSSTVASQSANHTHGTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYPEAQQSEPIAYFRLGLRVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCY
YTLCFRNEFQNLLLAIMLSATLTIPIWQWFTRFGKKTAVYVGIISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTPEPIFFSFYVFFTKFASGVSLG
ISTLSDLFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKKAL
QALRDEASSSGCSETDSTELASIL

FIGURE 13

GGGAAACGCAAAAGGCATACTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGCGTGCGGGAGCAGAGAGAACCTATGAAGCCCAGCAGTCTGA
GCCAATCGCTACTTCCGGGCCTACGGCTGGTCATGAGCCACGGCCATACATCAAACCTTA
TTACTGGCTTCCCTTTCACCTCCTGGCTTCATGCTGGTGGAGGGGAACCTTGTCTTGT
TGCACCTACACCTTGGCTTCCGCAATGAATTCCAGAAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATCCCCATCTGGCAGTGGTTCTGACCCGGTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTCTCATCTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATTGACGACTTCCATCTGAAGCAGCCCAC
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCAC
GAACCGAGCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTGTGAAGTTGAAACAGAAAAACCTGTTAGAA**ATGT**
 GGTGGTTTCAGCAAGGCCTCAGTTCCCTCAGCCCTGTAATTGGACATCTGCTGCT
 TTCATATTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCAGAAAAATGCTTATTGGGCAATGCTAAATATTGCGG
 CAGTTTATGCATTGCTACCATTATGTTGCTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAAACAAGGCTGGCCTGTACTTGAATACTGAGTTGTTAGG
 ACTTTCTATTGTGGCAAACCTCCAGAAAAACACCCCTTTGCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTGGTATGGGCTCATTATATGTTGTTCAGACCATCCTTCTACCAAATG
 CAGCCCCAAATCCATGCCAAACAAGTCTCTGGATCAGACTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTAGCATGCTGACTTGCTCATCAGTTTGCACAGTGGCAATTGGGACTG
 ATTTAGAACAGAAACTCCATTGGAACCCCGAGGACAAAGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCATTTCTTCTTGGTTTCTGACTTACATCGTGA
 TTTTCAGAAAATTCTTACGGGTGGAAGCCAATTACATGGATTAACCCCTCATGACACTG
 CACCTTGCCTTAAACAATGAACGAACACGGCTACTTCCAGAGATATT**TGAT**GAAAGGAT
 AAAATATTCTGTAATGATTATGATTCAGGGATTGGGAAAGGTTCACAGAAAGITGCTTA
 TTCTTCTCTGAAATTTCACCCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAAGCCATTGATAGATTATTCTAAAGGATATCATCAAGAACACTA
 TAAAAAACACCTATGCCATACCTTATCTCAGAAAATAAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMILNI
AAVLCIATIYVRYKQVHALSPEENVIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFOQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

FIGURE 16

CGGACGCTTGGCNGGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCGTATGCCGAGT
TCCGCTCTCGGGTCTTCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGGCTTCCGGAGAAAATCAGCGGTCTAATTAAATTCTCTGGTTGGTGAAGCAGT
TACCAAGAATCTCAACCCTTCCCACAAAGCTAATTGAGTACACGTTCTGTTGAGTACA
CGTTCCCTGTGATTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTCCCT
TCAGCCCTTGTAAATTGGACATCTGCTGCTTCATATTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGTTACCTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGGTCCGCCCCCGCCTGCCTCCGGAGTGCAAGTGAGCTCTCGGCTGCCCGCGGG
 CGGGGTGCGGAGCGAC**ATG**CGCCGCTTCGCCTCCTCTGGTCTTCGCCGGCTGCAC
 CTTCGCCTGTACTTGCTGTCACCGACTGCCCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCGTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTGAG
 GTCCTTCAGAGTAGCGGAAGGGACACCAGGCCTACGTGTTCTGCTCTTCGCGCGCCTA
 CCTCTACAAACAGGGTTGCCCAGCTCCCGCTCCAGCTTCCTGAATGTTTAGCTGGTGCCT
 TGTTGGCCATGGCTGGGCTCTGCTGTGCTGTGTTGACCTCGGTGGTGCACATGC
 TGCTACCTGCTCTCAGTATTTGGCAAACAGTGGTGGTGTCTACTTCCGTATAAAGT
 GCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAACAGCTGTTTTTCTATTGTTT
 TGAGACTTTCCCCATGACACCAAACCTGGTCTTGAACCTCTGGCCCCAATTCTGAACATT
 CCCATCGGCAGTTCTCTCAGTTCTATGGTTGATCCCATATAATTCTATCTGTG
 GCAGACAGGGTCCATCTGTCAACCTAACCTCTGGATGCTTTCTCTGGGACACTG
 TCTTAAGCTGTTGGCATTGCCATGGCATTAATTCTGGAACCCCTATTAAAAAATT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGTAATCATATACACAGTAGAAAAGA
 CACA**TGA**CTGGATTTCTGTTGCCACATCCCTGGACTCAGTTGCTATTGTAATGGA
 TGTGGCTCTAAAGCCCTCATGGTTGATTGCCCTATAGGTGATGTGACACTGTG
 CATCAATGTGCAGTGCTTTTCAAGAAAGGACACTCTGCTTGAAGGTGATTACATCAGGT
 TTCAAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCCTAGAAAATGCTGTTGT
 GGCGGGCGGGTGGCTCACGCCGTAAATCCAGCACTTGGGAGGCCGAGGCCGGTATTG
 ACAAGGTCAAGGAGTTCAAGAACAGCCTGGCAAGATGGTGAATCTGTCTAATAAAAAAT
 AAAAAAATTAGCCAGGCGGGTGGCAGGCACCTGTAATCCAGTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTGAACCAAGGTGGCAGAGGTTGCAAGTAAGCCAAGATCACACCAACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

M R P L L G L L V F A G C T F A L Y L L S T R L P R G R R L G S T E E A G G R S L W F P S D L A E L R E L S E V L R E Y R
K E H Q A Y V F L L F C G A Y L K Q G F A I P G S S F L N V L A G A L F G P W L G L L L C V L T S V G A T C C Y L L S
I F G K Q L V V S Y F P D K V A L L Q R K V E E N R N S L F F F L L F R L F P M T P N W F L N L S A P I L N I P I V Q F F
F S V L I G L I P Y N F I C V Q T G S I L S T L T S D A L F S W D T V F K L L A I A M V A L I P G T L I K K F S Q K H L Q
L N E T S T A N H I H S R K D T

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31.

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGGCGGGAGGAGGCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCATCATT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTCCGAAGTGCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTATATTGGAAGAC**ATGG**ATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAAACTTCAGAGACTTGTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
 CCCCCCGCAGTATCCTCTCCTTATAGTTGTGATTAAGGTTCTCGAACCTTGGGATTAATCT
 TGCTCACTGCTACTTTGTGATTCAACCTTCAGGCCATTAGCACCTGAGCCAGTGCCTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCTTGCCATTGCCAA
 GAAGTACATGTCAAGAAAATAAGGGAGTCTCTGCATGGGGGTGATGAAGACAGACCCCTTC
 CAGACTTTGACCCCTGGTGGACAACAGACTGTGAGCGAATGAGTCAGAGCCCATTCCGTCC
 AACTGCACTGGCTGCCCCAGAAACACCTGAAGGTGATGCTCTGGAAAGACCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGTCAAGACGGGAAAGCCCCCTGTTGGAGGAAGAGATT
 AGCATTGGTGTGCCAGTACCCCTGAGGCGACAGAAGGCTCTCTGAAGGGTTTCGCCAAG
 TGGTGGCGTGCTTCTGAGCGGGTCCATTCCATTCCATGGAGGAGACCTGCAA
 CAGATCACAAATGTTACGTGAGCTTCTGTTCACTCACCTGCCATTCCAAAAGATG
 CCTCTTAAACAAGTGTCTCTTCTCACCCAGAACCTGTTGGGGAGTAAGATGCATAAG
 ATGCCCTGACCTATTATCATTGGCAGCGGTGAGGCCATGTTGAGCTCATCCCTCCCTCCA
 GTGCCGAAGACATTGTCAGTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTAGCCAGAGGGTCCAGCCTTGGTCATCTGCGAT
 GGAACCGCTTCTCAGAACTG**TAGGAAATAGA**ACTGTCACAGGAACAGCTCCAGAGCCGA
 AAACCAGGTTGAAAGGGAAAAAATAAAACAAAAACGATGAAACTGAAAAAA

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FIGURE 20

MDLAANEISIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVY
KVLATGLLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLSIHIIHRLMSLPIAKKYSSENKGVPPL
HGGDEDRPFDPFWWTNDCEQESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPPFPWRRPLNRSQMLRELFPV
FTHLPFPKDAISLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHQSVA
I_EPGDYGVDTTTHWKVVIARGVQPLVICDGTAFSEL

卷之三

FIGURE 21

CCACGGTGTCCGTTCTCGCCCCGGCGAGCTGTCCCCGAGGCAGGGAGGAGCCCGAGGGCG
CGAGCCCCGATGAATCATTGTAGTCATCTTCAGTTCTAGCCGTTCAAGTTGTGATC
AAGGGACACGTGGTTCCGAACTGCCAGCTCAGAATAGGAAAATACTTGGGATTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAAACTTCAGAGACTGTTG
ATTGGTGAGACAGACGGCCATCAGTGTGGCATGTCAGAGAAAGGCAATTGAAAAATTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCCCAGTATCCTCCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTGGATTAAATCTGCTCACTGCCTACTTGTGATTCAAC
CTTCAGCCCCATTAGCACCTGAGCCAGTGCTTGTGGAGCTCAC

FIGURE 22

FIGURE 23

MSQFEMDTYAKSHDLMMSGFWNACYDMLMSSGQRQWERAQSRRAFQELVLEPAQRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAVALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELTP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVFYDGSTERVETEEGIGYDFRRP
 LAQLREVLRRFNLRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRQPQGPPIPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSRPQEMLRSAGLTQKWWQREISNFYLMQLNTIAGRNYNDL
 SQYPVFPWPVLQDYVSPTLDSLNPNAVFRDLSKPIGVNVNPKAHQALVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYHLIRVEPFTSLHVQLQSGRFDCSDRQFHSSAAAQARLESPADVKELIP
 EFFYFPDFLENQNGFDLGCLQTNEKVGDVVLPPWASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAAEELANVFYYCTYEGAVLDHVTDERERKALEGIISNFQGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIWFQHLDLKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPTMGSHKTQRLSGPWPVPGSGVSGQALAVAPDGKLLFSGGGHWDGSLRVTALPRGKLL
 SQLSCHLDVVTCIALLTCGIYLISGSRDTTCMVWRLLHQGGGLSVGLAPKPVQVLYGHGAAVS
 CVAISTELDMAVSGSEDGTVIITVRRGQFVAALRPLGATFPGPIFHLAGSEGQIVVQSSA
 WERPGAQVTVSYSLHLYSVNGKLRAISLPLAEQPTALTVDVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHV1VGLIEDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGGCTGGGCGGACCGTGGGGCTGTGAGAAAGTGCAATAATACATCATGCAACCC
 CACGGCCCACCTTGTGAACCTCTCGTGCCTGCCAGGGCTGATGTGCGCTTCAGGGCTACTCAT
 CCAAAGGCCATAATCCAACGTTCTGCTTCATCTGAAATCTATGGGTCTGGGGCTCTTC
 TGGACCTTAACGGTACTGCCCTGGCCAATGCGTCTCGTGGAGCCTTGCCTCCTT
 CTACTGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCCTCATCC
 GCACACTCCGTTACACACTGGGTCTATTGGCATTGGAGCCCTATCCTGACCCCTGTGCAG
 ATAGCCGGGTATCTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCCTGTAGC
 CCGCTGCATCATGTGCTGTTCAAGTGCTGCCTCTGGTGTCTGGAAAAAATTATCAAGTCC
 TAAACCGCAATGCATACATCATGATGCCATCTACGGGAAGAATTCTGTGTCAGCAGAAA
 AATGCGTTCATGCTACTCATGCAAACATTGTCAGGGTGGTCGTCCTGGACAAAGTCACAGA
 CCTGCTGCTGTTCTGGAGCTGCTGGTGGTCGGAGGCGTGGGGTCTGTCCTTCTT
 TTTTCTCCGGTGCATCCGGGCTGGTAAAGACTTAAGAGCCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCTGGGGCTATGTCATGCCAGCGGCTTCAGCGT
 TTTCGGCATGTGTGAGACACGCTTCCCTGCTTCTGGAAAGACCTGGAGCGGAACACG
 GCTCCCTGGACCGGCCCTACTACATGTCAGGCTCTAAAGATTCTGGCAAGAAGAAC
 GAGGCAGCCCCGGACAACAAGAAGAGGAAGAGTGAAGCTCCGGCCTGATCCAGGACTGC
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACCTGCCCTACAGGTCTCCATTGTGGT
 AAAAAAAGGTTTAGGCCAGGCGCCGTGGCTCACGCCCTGTAATCCAACACTTGTGAGAGGCTG
 AGCGGGCGGATCACCTGAGTCAGGAGTTGAGACCAGCCTGGCCAACATGGTAAACCTCC
 GTCTCTATTAAGATACAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAACGCTGAAACCCGGAGGCAGAGGTTGCAGTGAGGCCGAGA
 TCGGCCACTGCACTCCAACCTGGGTGACAGACTGTCTCCAAAACAAAACAAACAA
 AAAGATTTATTAAGATATTGTAACTC

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FIGURE 25

RTRGRTRGGCEKVINTSCNPTAHVNSSCPGLMCVFQGYSSKGLIQRSVFNLOIYGVLGLF
WTLNWVLALGQCVLAGAFASFYWAFHKPQDIPPFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPPVARCIMCCFKCCLWCLEKFIFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVVLDKVTDLFFGKLLVVGVGVLSSFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDELRNNNGSLDRPYYMSKSLLKILGKKN
EAPPDNKKRKK

009992524-111401

FIGURE 26

GAGTCTTGACCGCCGCCGGCTTGGTACCTCAGCGCAGGCCAGGCGTCGGCCGCCGT
 GGCT**ATG**TTCGTGTCGATTCCGAAAGAGTTCTACGAGGTGGTCCAGGCCAGGGTCC
 TTCTCTCGTGGCCTCGGACGTGGATGCTCTGTGCGTGCAAGATCCTCAGGCCTGTT
 CAGTGTGACCACGTCAATAACGCTGGTCCAGTTCTGGGTGGCAAGAACTTGAAACTGC
 ATTTCTTGAGCATAAGAACAGTTTCAATTCTCTACGCTAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTCACCTGATGAAGACACTATATTCTTGTTGTGACTCCATAGG
 CCAGTCATGTGTCATGTATACACGATACCCAGTCAGTAAACAAGATGA
 TGACCTGAAGTTCCGCCTATGAAGACATCTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTAGAGCCTCTGAGAAGCGCACAGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGGAGGCAGCGCGAGACTGGGAGGCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGTGACTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCATGTTGACTAACAGAC
 CAGTGGGTGCAAGAACAGATCACTCAAATGAAATACGTACTGATGTTGGTGTCTGCAGCG
 CCACGTTTCCC GCCACAACCACCGGAAACGAGGATGAGGAGAACACACTCTCGTGGACTGCA
 CACGGATCTCCTTGAGTATGACCTCCGCTGGTGTCTACACGCACTGGTCCCTCATGAC
 AGCCTGTGCAACACCAAGCTATACCGCAGCCAGGTCAAGCTGGTGTGCACTGGACAGAA
 CGCGTCCAGGAGTCTCTGAGACATGGCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCTTGAGGAGAATTGCGGGAAATGATTGAAGAGTCTGCAAATAAA
 TTTGGGATGAGGACATGCGCGTGCAGACTTCAGCATTCAATTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTGCCACCATGCTTGTGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTCATCCAGGCTCTGGACAGCCTCTCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACTCGCCAAGAACGAGCTGGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGCAACACTCGCATCTCCAGGGCTTCTGTACTGCTCTCATGGAGGGCAC
 TCCAGATGTGATGCTGTCTCTAGGCCGACATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCTTGATGTTGACAAAGAACCGGCCGTGCAAACCTGCTGCCCTGGTGTGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTGGGAGGGCTTGGAGAAGGCAGCGAAAGCACCAGCTCCGGA
 TGCTGCACAACCATTTGACCTCTAGTAATTGAGCTGAAAGCTGAGGATGGAGCAAGTT
 CTGGACGCACTTATTCCTCTGTCC**TAG**GAATTGATTCTCCAGAATGACCTCTTATT
 TATGTAACTGGCTTCATTTAGTTGAGTTGAGCTGATTGAGATGTAGAACCCATT
 TTTTATAAATAAAATGCTTATTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVLACACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINGANVDLILQPDDEDTIFFVCDSHRPVNVNLYNDTQIKLLIKQDD
LEVPAYEDIFRDEEEDEEHSGNDSDGSEPSEKRTRLEEEIVEQTMRQRREWEARRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSCNTSYTAARFKLWSVHGQKR
LQEFLADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKGMDRVTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSQTDHFQALDSLRSRNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAESTSSRMLHNHFDSLVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGCAGCGCCAGGCCTCGGCCGCGCTGGCTATGNTCGTGTCCGATTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GCTCTGTGTGCGTGCAAGATCCTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTCCAGTTCTGGTGGCAAGAACTGAAACTGCATTCTTGAGCATAAAGAACAGTTTC
ATTATTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTGTTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCTCTTTGGGTCTGGATTGGGACCCCTTCCAGTACCATTTCTAGTGAAC
 CACGAAGGGACGATACAGAAAACACCTCAACCCAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTGGCTATAAGAAAAAAGAAGAACGAAAAGAGACAGTTTTTGAAAGCTAA
 GTCTTCCTTATCGAGTCAGAACCCCCCCTTCITGAGCTATTACAGCTTTAACATT
 GAGTAAGTAGCCTCCGGTACCC**ATGGT**GACAGCCCCCTGGGTCCGGTCTGGGCAGGGCTC
 CTGCTCTTCTCTGATGTGAGATCCGTATGGTGGAGCTCACCTTGACAGAGCTGTGGC
 CAGCGGTGCCAACGGTGTCTGACTCTGAGGACCCCTGGATCTGGCCCATGTATCTCAG
 CCTCTTCTCCGGCCCCCCCACGCCCTGCCATGAGATCAGACCTTACATTAAATACCATC
 CTGAAGGGTACAAAGGGGACCCAGGCCAATGGGCTGCCAGGGTACATGGGAGGG
 TCCCCAAGGGGAGGCTGGGCTGGGAGGCAAGGGTGTGGACAGGGGGAGATGGGAGCCCC
 GCGCCCCCTGCCAGAACGCGCTCTCGCTCTCACTGGGCCAAGACGCCCTGCACAGC
 GGCAGGACTTCCAGACGCTGTCTCGAAAGGGTCTTGTGAACTCTGGGTTGA
 CATGGCAGCAGGGCAGGTGGTCTGGCTCCCTGCTGAGCATCTACTCTCAGCCTCAATGTC
 ACAGCTGAAATACAAGGAGACCTAGTCAGTCACTTACATGACAAAGGGAGCTGTGTCATC
 CTGTAACGGCAGGGCAGGCCAGGACCATCATGACAGACGAGCTGTGATCTGGGACTTGC
 CTACGGGACCGCGCTGGGTCGGCTTCAGGCCAGCGAGAACGCCATCTACAGCA
 ACGACTTGACACCTACATCACCTTCAGGCCAGGCCCTCATCAAGGGCGAGCAGACT**TGA**GGG
 CCTCTGGGCAACCTCCGGGCTGGAGACGCTCTGGTCTGGTCCCTGCGACCTCG
 TTGCACTGAGGACTGGAGACAGGAGGGCAGGAGTCCCGGGAGCTGGCATTCTGGGAGA
 CCCTGCTCTATCTGGGCGCATCATCCTCCAGCCTATTCTGCTCTCTCTCT
 TGGACCTATTAAAGAGCTGCTAACCTAAATCTTAGAATTCTCCAGGCTCGTAGGCC
 AGCACTCTCAAATTGGAAATGCTGGAATCACCCGGGTTCTGTTAAATGCGAGATTCT
 GACTCAGCAGGTCTGAGTGGGTCAGGATTCTGTTCTCATATGTTCTGGGTGATGCTG
 ATGGGGTCACTGAGGACTAACACTGGACCAACAGGTTCTGAGATTCTCAATATCTG
 TACTTTCTGACATTCTGGGAATCTCCACCATCTGAGAATTCTCCAACTATTCT
 TGAGACAGACTCTGCTGTGGCCAGGCTAGAGCTGGCAGTGGCAATCTCGTTCACTGC
 AACCTCTGCTCCGGGCTCAAGCGATTCTGGCTCATCTGGCTCAGGCCCTCTGGGATTAC
 AGGGCGCTCTGACCTGGCTCTGAACTCTGACTTCAGGTGACCCACCCGGCTCTCAAC
 TTGGGCCAGGCTGGTCTGAACTCTGACTTCAGGTGACCCACCCGGCTCTCAAAAT
 GCTGGGATACAGGTGAGGCCACCGTGCCTGGCAATTCAACATTCTTAAATCTCTCAT
 CCCTCCAGGGCTCCGGTCTGATCTCTTACCCCTTCCCTCTGGCTCAGGCC
 TGCACCATCTGCAAGGCCAGGCTCATTTCTGATCTAAACACTGAGGACTCTACTGCT
 GGGTCCGGGAAGGGTGAAGGGGGCTGAGACAGGCCCTGCCTGGCCAGGCT
 GTCCAGGCCAGGGAGAGATGTGTCATAGGTTAAAGCAGACCCAGAGCTCATGGG
 GCCTGTTCTGGGTTCTGGTCTGCTGCTCTCCATTACCCACTGCTCCAGGCC
 TGGGACGGGCTCCGGTGGCAGGGCAGGTATCTTCTCCGGTCTCATCCACCTGGCAG
 TGCTCATGTTACAGCAACACCCAGGGGCCCTGGCAGGTCAAGGGTTCTGAGGAGAGG
 ACCCAGGAGTGTGGGGGATTGGGGGTGAAGTGGCCCCGAAGAATGGAAACCCACACCA
 TAGCTCTCCCCAACACTGATACGGCATCTGGCAGAGAACACTGCCCTCACTGGGATCCC
 CTTCCTGCTCTCCAGGGCTCTCAGGCTGCCCTCAGACACTGATGTCCTGCCCCAGGTGCT
 CTCTGCCCTCATGCCCTCACCAGGGCAGTGGCCGACTCTCCAGGCTTATCAAGGTG
 CTAAAGGGGGGGTGGGAGCTCTGGCTCATGCCCTCAGGCTCTCCGGGCTGGTCTGCCCTTAC
 AAACACCTGCAAGGAGAAGGGCACGGAGGCCCAAGGTTAGAGCCCTCAGCAAGGTCTGGG
 AGCTAGAGCAAAAGGAGGGGACCTCAGGCCCTCCGTTCTCTCCAGGGTGGGGTGGCCTGGT
 GTTCCCTAGCCTTCAAAACAGGTGGCTGCCCTCTCCAGGGAGGGGGCTGGCCTGG
 CCATTGGTCTCATGAGACTCTGGGCTGAGGTGGCCCGGGGGTGAATCTGGTGTCTCAC
 AGCCGAGGGAGGGCAGTGGCTCCATGCCAGTGCAGAACAGGGTGTGACCAAGTGGCAGGA
 AGACCTGCTATAACCACCTGCTGATCTGCCCTGCCCTGACCCGGCACGCCCTGCC
 GTCCAGCATGATTAAGAATGCTCTCCCTTGGAAAAAAAAAAAAAA

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPPGQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDE

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

T07777-Y2526960

FIGURE 31

ACTCGAACGCAAGTTGCTTCGGGACCCAGGACCCCCCTGGGGCCCACCCGCCAGGAAAGACTG
 AGGCCGGCCTGCCCGCCGGCTCCCTGCGCCGCCGCCCTCCCGGACAGAAGATGTG
 CTCCAGGGTCCCTCTGCTGCTGCCGCTCTGACTGGCCCTGGGGCTGGGGTGAGG
 GCTGCCCATCCGGCTGCCAGGTGCAAGGCCACAGACAGTCTCTGCACCTGCCGCCAGGG
 ACCACGGTGGCCCCGAGACGTGCCAACCGACAGGGCTGTACGTCTTGAAGAACGGCAT
 CACCATGCTCGACGCCAGGGCAGCTTGCGGGCTGCCGGCTGCAGCTCTGGACCTGTAC
 AGAACCAAGATGCCAGGCCAGGGCTTCCAGGCCACTGCCAACCTCAGCAACCTG
 GACCTGAGGCCAACAGGCTGATGAAATCACCAATGAGACCTTCCGGCTGGCGCCCT
 CGAGGCCCTCACCTGGCCAAGAACGCCATGCCACATCCAGGCTGGTGCTTCGACACGC
 TCGACCCGCTCCCTGGAGCTCAAGCTGCAAGGACAACAGAGCTGCCGGACTGCC
 CTGCCCCGGCTGCTGCTGCCACAGGCCACAGGCCCTGGGGCTGGAGGCCGGCAT
 CCTGGACATGCCAACCTGGGCCCTGCCAGCTGGCTGGTGCTGGGCTGCAGCAGCTGGACG
 AGGGGCTTCAGGCCCTGCCAACCTCACGACACTGGATGTGTCGACAACCAGCTGGAG
 CGAGTGGCACCTGTGATGCCAGGGCTCCGGGGCTGACGCCCTGCCGGGAAACAC
 CGCATTGGGACAGTGGGCCAGGGGGCTGCCACAGGCCCTGGCTGCCCTGCAAGGACTGGATG
 TGAGCAACCTAACGGCTGCCAGGGCTGCCACAGGCCCTCTGGGGCTTCTCCCCGCCG
 CTGCTGCCAGCTGCCAACCCCTAACCTGCGTGTGCCCTGAGCTGGTTGGGGCTG
 GGTGCCGAGGCCAGCTCACACTGCCAGGCCACTGGAGGCCAGGGCTGCCACCTCCGCCA
 AGAACGGCTGCCGCTGCTCCGGAGCTTAGCTGACTACGCCACTTGGCTGCCAGGCCACACC
 ACCACAGCCACAGTCCCCACCACGAGGGCCGTGGTGCGGGAGGCCACAGCCTTGCTTCTAG
 CTTGGCTCTACCTGGCTTAGGCCACAGGCCGCGCCACTGAGGCCCTGCCGGCC
 CTGCCCCACCAGACTGTAGGGGCTGCCCCAGGCCAGGACTGCCACCGTCCACCTGCTC
 ATGGGGGACATGCCACCTGGGACACGCCACACTGGCTGCTTGTGCCCGAAGGCTT
 CACGGGCTGACTGTGAGAGGCCAGATGGGGCAGGGACACGCCAGGCCACCCACT
 CGCCGAGGCCACCCAGCTGCCCTGAGGCCACTGGCTGAGGCCAGGCCACCTCCCTGCC
 GTGGGGCTGCACTGCCAGGGAGCTGGCTGAGCTGCCACGGGCTGCCACCTGGCTGCC
 TCGCAACCTATGGGGCTGTATAAGGGCTGGTGAACCTGCGACTGCCCTGCCCTGCTG
 AGTACACGGTCAACCGACTGCCGCCCCAAGGCCACTTACTGGCTGTGCTGATGCC
 CCCGGGGGGCTGGGGGGAGGGGGAGGGCTGCCGGGGAGGCCACACCCCAAGGCC
 CTCCAAACAGCCCCAGTCAACCGAGGCCCGAGGGCAACCTGCCCTCTCATTGCC
 CCCTGGGGGGGTGCTCTGGCCGCGCTGGCTGGGGGGAGGCCACTGTGTC
 GGGGGGGCCATGGCAAGCAGGCCACTAGGGACAAAGGGCAGGTGGGGCCAGGGGG
 GGAACATGGGGGGAGTGAAGGTCCCCCTGGAGGCCAGGGCCAGGCCAAACAGGG
 AGGGCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTCCAGGGCTGCC
 CAGTCACCCCTCCACCCAAAGGCCACATCTAAAGGCCAGAGAGAGACAGGG
 GGCTCTCAGCCAGTGAAGATGGCCAGGCCCTCTGGCTGCCACACAGCTGGGGCG
 CAACCTGGGGATGTGCAAGCAGGGCTGTGAGACAGCTGGGGCTGCTCCCTG
 CCTGGCTCTCTCATGTGAGATGCTGTGCCAGCTGACGCCCTAACGCC
 CGAGTGGCTATGAGGACAGTGGCTGCCCTGCCACAGCTGAGTCCCTGGGCC
 GCCCTGGCATGTGCTGTAACCGATGCCCTGGGCTCTGCTGGGCTCTCCAC
 CCTGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAGCGGGTAG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGGAACACTGGAAAG
 GAGATGCTTAAATATATATTATAAGAGATGCCCTTCCCATTTATCTG
 GGAAGATGTTTCAAGACAGAGCAAGGACTTGGTTTGTAAAGACAAACGATG
 AAGGCTTTGTAAGAAAAAATAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVPILLPLLLLLALGPGVQGCPSPGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN
GITMLDAGSFAGLPGQLLDSLQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLLLELKQDNELRALPPLRPRLLLLDLHSNSLLALEP
GILDGTANVEALRLLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRRLAG
NTRIAQLRPEDLAGLAALQELDVSNISLQALPGDISGLFPRLRLAAARNPNFCVCPLSWFG
PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVREPTALS
SSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPE
GFTGLYCESQMGQGTRSPPTVTPRPPRSLTGIEPVSPSLRVGLQRYLQGSSVQLRSRL
TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAQDKGQVGPGAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

FIGURE 33

FIGURE 34

MRLIRNIYIIFCSIVMTAEGDAPELPEERELMTNCNSMSLRKVPADLT PATTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQQLDLKT FEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTMCICEAGNMSHLEILGLSGAKIQKSDFQKIAHLHINTVFLGFRTLPHYEEGSLP
ILNTTKLHVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSENAKTSVLL
LNKV DLLWDDLFLLQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLTISNAQMHPHMLFPNYPYPTKFQYLNFANNILTDELFKRТИQLP
HLKTLILNGNKLETLSVSCFANNTPLEHLDLSQNLLQHKNDENCSPETVVNMNLSSYNKLS
DSVFRCPLPKSIQILDLNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRSLSVLNIE
MNFI LSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLI TIVVIMLVGLAVAFCC LHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLSPNFVQNEWCHYE FYFAHHNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTCTGGCTTGCTGTTGAAACACCTGCCCTCCAAAGGACGGCCCTGGAGGGTCGCCGGAAAGG
 GAGGGAAAGGAAGGAGGGCGGGGCCGCCCTGCCGCCGCCGCCCTGCCGCCCTCTGGCGCCCCCTGTCCGCCGGC
 CCAGCCCAGCCAGCCCCCGGGCCGGTCRACAGCGCAGGCCAGCGGCCGCCCTCCCGGCCCAAGCGGCCGC
 CTGCTGCCCCCTGCCCTTGCCCCGCCAGCTTCTGCCGCCAGGCCGCCGGCGGCCCGGTGACCGTGA
 CCGTGGCTTGGCGGGCGGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAG
 CTGGCAGTGAACCTTGCCCCGGTGCAGGCCAGGGCCAGCCTCAGGAGACCTGTGATTATACGGGAGAGAT
 CTGGAGCCGGAGGCCACTACCCGGGGCCGGAGCCGAGCTCGAGAACCTTCTCCGGCCGTCGCTGCCGG
 CGGGGAGGGAGTGGGAGCGGGCCAGGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC
 AACAGGGAGAAGTCGGCTCGGCTCGGAGGCCCTCCACGGTAACACAGCAACAAAAGGTTAGAGAACAGAG
 CTCTGAGAAGGCTGCCAGATGATCACAGTGTGGCTGTGGCTGAAGATGTAGAGAACCTGAGCTGGCC
 TTGGCTGAAACCTTAAAAATCACAGCTTCTAGCTCATGGCTTACGGCTTATGGCTGGGGCA
 CATCGAGGGAGACTCACATCCAGGCCGATTATGAAATGTTATGACGGAGCTGTGGCTCATCTACTAAGGG
 AAATGAGGCTCCAGCTGGAGGAGTGGATTAGTGGCTGCCGCTGACCAGATTCACTGGTGTCA
 GGAACCTCCCTGGCTGAGTGTACTGGTGCACATCTAAAGGTCATGGTGCACATGACAGGCCACAGCTGGGTC
 ACTGTTAAAGATGGATCTGGAGACATGATATTGGAGGAAACAGTGGAGAACAGGAGATCCTGTCTCAATGAGC
 ACCCTCCCGATGGTGGCCGCTACATGCCATAAACCTCTACCTCTGGTTGATAATGGGAGCATCTGATGA
 GAATGGAGATCTGGGCTGCCACTGCCAGATCTTAATAATTATTAATACCGCCGGAGAACGAGATGCCAACCT
 GATGAGCTGGAATTAAAGCACCAAAATTAAGGAAATGCCAGTGGTGAAGATGTGAAAGTTGTAATGTGTC
 CAATATCACCGAAATTACACATTGGAAAAGGCCACAGGGCTGAGCTGTATGCTGTGGAGATCTCAGATC
 ACCCTGGGAGCTGCTCTGCTGTGGCTGAGCTTCAGGGACTCTGGTGCAGGAGTACTGGGCCGAATCTGGC
 CGGGAGCTGCTCTGCTGTGGCTGAGCTTCAGGGACTCTGGTGCAGGAGTACTGGGCCGAATCTGGC
 GGTGGAGGAGACCGGATTACCTCTCCCTCCCTCAACCCCGATGCTACGGAGAACGCCCTAAGGGGG
 CGGAGCTGGGAGCTGGCTGCTGGAGCTGGAGCTGGAGCTGGAGATGACATCAACAAACATTCTCTGATTIA
 AACACGGCTCTGGGAGCAGAGGATGACAGATGCTCCAGAAAAGTCCCAATCACTATATTGCAATCCC
 TGAGTGGTTCTTCGCGAAATTCGACAGCTGGCTGCCGAGCAGCAGCTGGCTGAGCTGGTGGAAATAATCC
 CTTTGTGCTGGGCCAACCTGCAGGGGGCGAGCTGGCTGGCTGAGCTGGCTACTCCATGCTGGGGTCCCC
 TGGARAGGCCAACACCCCCCCCCCGATGACACCGTGTCTGGCTGAGCTGGCTACTCCATGCTGGCTCCAC
 ACACGGCTCATGACAGCACCGGGAGGGGGTGTGCCACAGGAGCTTCCAGAGGAGGGGACTCTGG
 ATGGGGCTCTGGCACACCGTGTGGAGACTGTAACGATTTCTAGCTACACTCATACAAACTGCTCGAACATG
 TCCATCATGGGCTGTTGATAAAATACCCCATGAGAGGCCGCTGGAGGAAATACCCGGGGAT
 TCTGATCTGTTCTGGCACAGGCTCATCTGGCTTAAAGGCTGGTGAAGAGATTACATGGAAAGGAAAGATTCC
 CAAACCGCATTATCTGGTGAAGGCTTACACATGACATGCCAGAACGCCAACGATGGGATTACTGGGCCCT
 CTGAAACCTGGAGAGTGTGGTGTACACAGAACGGCGAGGTTACTGCACTCCACCAAGAAACTGTATGTTG
 CTATGACATGGGGCCACAGGTGTACTTACATGGAAACCAACATGGCCAGGATTCGGAGAGGATCATGG
 AGAAGTTGGAGGAGCAGGGCTGAGCTGGCAGGGCGCTGAAGCTGGGGGGCGAGAGGAGACAGCCT
 GGGTGAACCTCTGGGCCCTGAGACTCTGCTGGCACAGGCTTGAACATGGTACTGGCTCATAG
 TGGACTCACTGGTGTCTCTGTAATCAAGAGTGGCTGGAGAGGAGGGTGTGGAGCAGGTT
 CAAAAGGGAGGGTGGAGGTGGGGCTTCTTCTTTCTTGTGCTTCAATTACAAATACTGGACAGACA
 GCAGAGAAAAGCTGATGGGAGTGGAGAGACTCAGCAAGGCCACCTGGGAATCAGAGAGAGAAGGAGGG
 GAGCTGCTGGTGTGGAGGAGGGAGGGCTGGCTGAGGAAAGGATTCCTGGCTTCCCTGTTGCTGGAG
 GTTCCACGGTGTGGCTTCAATTGCAAGCTAAATTGCACTTCCCAGGGCTGGCTGCTCCAAATGTTACCA
 TTTGAGATGCTCCCAAGGGCTCTAAAGGAAATCCACCCCTCTGGCCCTGGGACATTGCAAGCTGACAATAA
 ATTCTGTGTTCTTCTGACAATAGGGTCACTGGCAAGTCACATCAGTAGGCTTCTGAAATCTTGTGTT
 TTTCAACAAAGGAGTGTGTTCAAGGGAGAGAGGGCTGAGATCATTGAGGAGCTTGTGAGGAG
 TGGAGCTTCTTCACAAATCTGGGTCATAAACAACCCCAAGTCCCTGCTGATCCAGTGGAGCTTGTG
 CCCAGGTAGGGAGGAGGCCAGGGCTGAGGAGGGCTGAAGGCCCTCTCTCTGAGGTTATGGCCCTGTG
 CTGCTAGGACTGGAAAGAGGGAGGGCTGAGGAGGGCTGAAGGCCCTCTCTGAGGTTATGGCCCTGTG
 GAAATTGAGTGTCTCATGGTGGCTCATATCAGCTGGGAGTTATTGATGATGAGATGCCAGATCTCCA
 GATTAGGCTAAATGTAATGAAAACCTCTAGGATTATCTGGAGCATCAGTTGGGAAGAATATTGAAATT
 CTTGCAAGAAAAAGTATGCTCATCTTGTGTTAATGTTGCTGCTCATGGCTGGGAAATAATGAAA
 AATAAAAGCAATGGTAAAGGCCCTAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEITWSREPYYARPEPELETFSPPPLP
AGPGEWERRPQEPRPKRATKPKKAPKREKSAPPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPMVARYIRINPQSFDNGSICMRMEILCPLDPNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHGEHEVGEPEF
HYIAGAHNEVLGRELLLLVQFVCQEYLARNARIHLVEETRIHVLPSSLNPDGYEKAYEGG
SELGGWSLGRWTHDGINNNFPDLNTLLWEAEDRQNVRKVPNHYIAIPEWFLENAATVAA
ETRAVIAMKEIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSSHKGKIPNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSPLPARR
LKLRGRKRQRG

FIGURE 37

CTAAGAGGACAAG**GAT**GAGGCCGGCTCTATTCTCTAGGCCCTCTGTTCTCCGGCAAGCTGCAGGG
 ATTTGGGGATGTGGGACCTCCAATTCCCAGGCCCGCTTCAGCTTTCCAGGTGTTACTCCAGCTCCAGC
 TTCAAGCTCCAGCTCCAGGTGGGCTTCAACCTCCAGGCCAGCTTAGGCAGCGGAGGTTCTGTCCCCAGTTGTT
 TTCAATTACCGCCCTGGTGATGACCGTGGGACCTGCCAGTCAGTTCTCCGCCAGACACCACCTTC
 CCGTGGACAGAGTGGAACGCTTGAATTCAACAGCTCATGAGGTTCTTCAGAAAGTTGAGAAAAGAATTTCTAA
 GTGAGGAAATATGTCATTAAATTAGTGTGATGAAACAAACTGTAAACCTAAGTGTGCAAGATGACATCAT
 GGAGAAGGATAACATTTCTACACTGAAGTGGACTCTGGAGCTGATCAAGGTGAAAGTGAAGGAGATGGAAAAAAC
 TGGTCATACAGCTGAAGGGAGTTTGTGGAAGCTCAGAAATGTTGACCGCTGGAGCTGAGATAAGAATT
 ATGACTCTTGGTAGAGAACCTTGAAGACACTGACAAACAAACATGTCTGGCATTGCGCAGAAATGTC
 TCTGAAGAACAGCTGAAAGAGTGTGGAGCTCTAAAGATCAAAACCCCTGTGTCACCCACTC
 CAGGGAGCTTGGTGTGGTGTGGTAACGAGCTGGTGGGTT
 TCTTATCTATGGTGTGGGCTAGGGATTACTCTCCCAAGCATCCAAACAAAGGACTGTATTGGGTTGCCCC
 ATTGAATACAGATGGGAGACTGGTGGAGTTATAGACTGTACACAAACACTGGATGATTGCTATGTATATA
 ATGCTCGAGACTGGGATCTGGCATACCTTGCCCAAGGTGAGCTGAGCAGTTAACACAAACATGTACGTCAC
 ATGTAACACACCCGGAAATTGGCCAGAGTAACTTGACCCACACAGATTGCTGTGACTCAAACACTCTCTAA
 TGCTGCCATAATAACCCCTTATCATATGCTATGTTGCTTGGCAAGATAATTGACTTTGCTGGGATGAGAATG
 GATTGTGGGTTATTATTCAACTGAGGCGACTGTGTAACATGGTGGATTGATAACACTGACACCAACACT
 CAGGTGCTAACACACTGGTATACCAAGCAGTATAACCCATCTGTTCTAACGCCCTATGGTATGGGTTCT
 GTATGCCACCGCTACTATGAACACCCAGAACAGAGATTTTACTATTATGACACAAACACAGGGAAAGAGG
 GCACAACTGACATGTAATGCTAAAGATGCGAGGAAAGTGGCAGGACTTAACTATAACCCCTTGGAGGAGAAA
 CTTTATGCTATAACAGTGTGTTACCTCTGATGATCTTCGTCAGCAGGCTCAG**TAA**GGCTGTTA
 GGAGTTAGGGTAAAGAGAAAATGTTGTGAAAGAAAATGTTCTCTCCACTTACTTAGATATCTGAGCTTGT
 CTAAAGATGTGTTCATTTGCGACCATGTTAGGTGCTAGTTACACACATAGAGATCTAGGACATTGGTCT
 TGATTGTGAGTTCTCTGGGAACTATCTGCTCTCAGGCCATTGCGATAAAAGCTGCTGTAGGGTGGG
 TTGTCAGGGTCAAGGGCACTGGGGCTACTGAGGCTTCACTGTGGAGGAGCTTCACTAGAGGCTTAAATA
 GGAATTAAAGAACCTAAACACTGAGTGGCTTCTAGGATTCTGTACAGGAATAATTGCCCAACTGATGTC
 CTCATCCATGTAGCACCACTTAATTCTTCCATGCCGAAACCTGGGGACTTAGTTAGGTGAGTTAATA
 GGAGCTCTCGAGGGACCAAACTTCAACTTTTCTCCCTCACTGACCTGGAAATGTGCTGTGTT
 CAGATAAGTAAATTGGCATGCTTATATACATCTGTAAGTGTGAGTTTATGGAGAGGCCCTTTT
 ATGCAATTAAATGTACATGGCAAAATAACCCAGAAGGATCTGAGATGAGGCCACTGCTTTTCTCTC
 ATTGTCACCTACTAAAGTCAGTAGAACTCTCATACCTCTCCAAAGGCAGCTCAGAAGATTAG
 AACCAAGACTTAACTAACCAATTCCACCCCCCAACCAACCCCTTCACTGCCFACTTTAAAAAATTAATGTT
 CTATGGAATCTAAGTGAATTAAATTCTTCTTAACTGACTGTTCTAAATAAGACCTGGAGCATA
 AGACTTAAAGAAAATCTGATGGCAGTGACAAACTGCTAGCATTTATTGTTACTAAATAAGACCTGGAGCATA
 TGTCACCTATTGAGTGTACTGAGTGTGTTGCTTGTGTTAAGCTGGAACCTGTAAGAATTGTAAGAAAAT
 GAAAATTAAATTTTTTCTAGGACGACTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTCAGTGT
 TGGAAACCTTGTGGTGTGATGTGCTCTGTGCTTTGAAATGACTTTATCATCTAGTTGTCTATT
 TCCCTTGTGTTCAACTCTAGTCTATGAGATTGGCAGTTAAATGCTTACTCCCCCTTAAATAAAATGAT
 TAAAATGTGCTTGTGAAAAAAAAAAAAAAAAAAAAAA

FIGURE 38

MRPGLSFLALLFFLQQAAGDLGDVGPIPSPGFSSFPGVDSFFFSSSRGSSSSRSLGS
GGSVSQLFSNFTGSVDRGTCQCSVSLPDFFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPTPGSCGH
GGVNVISKPSVVQLNWRCFSYLYGAWGRDYSPQHPNKGLYWVAPLNTDGRLLYYRLYNTLD
DLLLYINARELRITYGQGSGTAVYNNNMVNMYNTGNIARVNLTNTIAVTQTLPNAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCGVLYATRTMNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPO

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCCTCCAGGGAGCTGTGGTCATGGTGGTGGTGAACATCAGCAAACCGTCTGT
GGTCAGCTCAACTGGAGAGGGTTTCTTATCTATGGTGCTTGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTGCTATTGTATATAATGCTCGAGAGTT
GC GGATCACCTATGCCAAGGTAGTGGTACAGCAGTTACAACAAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

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FIGURE 40

TCTCGCAGATAGTAAATACTCGGAAAGCGAGAAAAGAAGCTGTCTCCATCTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGGAG**ATGGGGAGCGCTCTGGGGCTGTGCTCCATGGCGAGCT**
 GGATACCATGTTGTGAGGAAGTGC^CCCCGTGTTCCTATGCCGATGCTGTCTAGTGAAAC
 AACTCCACTGTAACTAGATTGATCTACACTTCTGTTGTGGAGTATGTAGCTTG
 TGTAATGTTGATACCCAGGAATGGAAGAACAACTGAAATAAGATCTGGGATTTTGTGAGAATG
 AGAAAGGTGTTGCCCCCTGAAACATTGTTGGCTATAAAGCTGTATATGTTGTCTTT
 GGTTTGGCTATGTTCTCTCTCTTACTAATGATCAAAGTGAAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTCACAACTGGATTTCGGTTCTTAAATTCTGTCGACCAATTGCAATT
 TTATTGGGCATTCTCATCCAGAAGGAACCTTACAACACTGTTGCTGGTTATGAGGCATG
 GCAGGGCCTTTGTTCTCATCCACTACAACACTGCTTACTATGATTTGCAACATTGAT
 GAATGAACTGTTGGGTTGAAAAAAATGGAAGAACAGGAACTCGAGATGTTGGATGAGCCTG
 TATCAGCTACAGCTGTAATATCTGCTGTTAGTGTCACTGCTGTTCTGCTAC
 TACACTCATCCAGGACTGTTGCAAGAAAACAGGGCTCATCAGTGTCAACATGCTCTG
 CGTTGGCTCTGTATGTCATACTGCCAACTTCAAGAACTCACAACCAAGATCTGGT
 TGTTACAGCTTCACTGAAACATGACTGCAACAACTGTTTGGATGAGCTGTTGCA
 GAACCGAGAACAAATGCAACCAAAGTCTACTAAGCATTAATTGGCTACAATACAAACAGCAC
 TGTCCTTAAAGGAAAGGGCAGTCAGTCAGTCAGTGTGGCTGTCAGGAAATTAGGACTAATTC
 TCTTTTGTGTTGTTGATTTTTCACATCGCATCGTACTTCAACAACTAGTCAGGTTAATAAA
 CTGACTCTAACAAAGTGTGAACTCATTTAGAAGATGGTGGAGCTAGGATGTGAGTC
 ACTGGAGGATGGGGACGATGTTGCACTGGAGCTGTAAGATAATGAAAGGGATGTTGCACTTACA
 GTTATTCTCTTCTTCACTTCACTGTTCTGGGTTCACTTATATCATGATGTTGCA
 AACGGGTGCACTGATGACCCCTCTGGTGGATGAAACACTGAGCTGAGCAGCTCTGGTGA
 AATCTCTTCACTGTTGGATGGCATCGTGTATGTTGGACACTCGTGGCACCACTGTTG
 TTACAGCTGATGTTGACTTGTGAG**TAAGTGTGAGACTCTACATGAAAGTCCCAC**TGTTGATTATG
 TTATTGAAACAGTATCTCCAACTTTGTAAGTTGTTGATGTTGCTGTTCTCATGTAAC
 TTCTCCAGTGTCTGGCATGAAATGATTTACTGTTGCTGTCATTTGTTATTCTTACCAA
 GTGCAATTGATATGTAAGTAAAGTGAATTGCAAGGAAAGTTTATGAATATGTTGATGAGT
 TAGTAAAAGTGGCCATTGGGCTATTCTCTGCTCTAGTTGTAAGGATGAAATGAGGATTA
 ACAAAATTTGTTGACTATTAAAATTATTAAGCTTAAAGCTTCTTACGAAAGCTTAAA
 GCAAAATGTTGGCTGCTTTGAATATTGATGTTGCTGGCAGGATCTGCAAAAGAAC
 ATGGTTTATTAAAATTAAACAAAGTCACTTAAATGCAAGGTTGCTGAAATACCTTATA
 AGGTTTACCTCTGATCGGAATTACACAGTGGAGGTGTTAGTGGACAAATAGTCAGG
 TTATGAGATGGAGTGTGGTCAACTTAAATGAAATACGAAATATAAATCTTACTGGGTAGAGA
 TGGCCTTGGCAACAAAGTGAACTGTTTGTGTTAAACTCATGAGTATGGGTTCACT
 GGAATGTTGGCAAGTCTGAGGATTAGCAAGGATTGAAAGGATAATCTGGGTAGAGA
 AGGAAGTGTGTTGAAAGTCACTTGGAGTTGAAAGTGTGTTGGGCTGGCCACGGTAC
 GGTAAATCCCAGCACTTGGAGCTTAAAGTGGTAGATTACTGAGCCCAGGAATTCAAGACCA
 CCTGGCACATGGTAACCTGTTCTATAAAAATATCTGGCTTGGCATATGCTGTGTC
 CAGCACTGAGGGCTAGTGAAGATGCTGAGCCCAAGGCCAAAGGTTGAGTGAAGTCA
 CGTCACTGCACTCACTGGCAGAGTAAGCCAAAAAAATATATATATGAAATCAAGG
 AGGCAAAATTGACAGGGAAAGGAACTGCAAAACCACTAGGCTTGTAGTGGTACTTAT
 ATAAAATCTAGTCCAGTTCTCTCATTTAAAATGAAAGACAGTGAATACAGACTTAA
 GCTCAGATAGCTAATTGAAATTTCAGTGTGCAATTATGACCTCTCTGACATTAA
 AAATAATTCTATTCAAATACATGCAATTGATTACACCTCATACTGTGATAATTAAATG
 GATGTGGAATGCTGGTGTCCAGCATGACCCATAAACAGGTGAGAAGATGTTGTT
 AGAATAAAACTCTGCTTATAGTAACTACACAGTCAAAAGATGTTAAAATGCTTTGTAT
 TTACTGCCATGTAATTGAAATATAGATTGTAACCTTCAACCTGAAATACAGCAGT
 ATGAGAGTTGTTAGTTATGATGTCAGTGTCAATGAAAGCTTTAAATCTACAAAT
 TCTCTTAAAAATATTATGAAATGGAATATAACAAATTGAGCTTAATCTCCCAACC
 TTATTCTGTGTTGAGACATTGTTACCTGATTCACAAATTGATGGCTGTTTACCTCTAAATAA
 ATGAATTCAAGGAGAAAAAA

FIGURE 41

MGSVLLGCSMASWIPLCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGYKAVYRLCFGAMFYLLSLMIKVKSSEDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGFTTVWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKM
EEGNSRCWYAAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFIGISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSSLIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVWVKISSSWIGI
VLYVWTLVAPLVLTNRDFD

FIGURE 42

GCGAGAAAGCTGTCATCTTGTCTGTATCCCGCTGCTTCTTGNACGTTGTGGAGAT
GGGGAGCGTCCCTGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTGTGTGGAAGTGCC
CCGTGTTGCTATGCCGATGCTGCTTAGTGGAAACAANTCCACTGTAACTAGATTGATCTA
TGCACCTTCTTGCTTGGAGTATGTGAGCTTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTGTGAGAAATGAGAAAGGTGTTGTCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTGTGCTTGGTTGGCTATGTTCTATCTTCT
CTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTCACAATGGAT
TTTGGTTCTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAAC
CANGTTGTGTGGAAGTGCCCCGTGTTGNTATGCCGATGCTGCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTNTTGCTTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCCCTGGATTTGTGAGAATGAGAAAG
GTGTTGTCCTTGTAAACATTTGGTTGGCTATAAAGCTGTATATNGTTGTGCTTGGTTG
GCTANGTTCTATNTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTGGTTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGCCAGTGGAAACAACTCCACTGTAACTAGATTGATCTATGCACTT
TTCTTGCTTGGAGTATGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACT
GAATAAGATTCTGGATTTGTGAGAATGAGAAAGGTGTTGTCCTTGTAAACATTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTGGTT
CTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGAAACAANTCCAACCTGTAACTTGGATTGATCTATGCACTTTTCTTG
CTTGGTAGTATGTAGCTTGTGAATGTTGCCAGGATGGANGAACACTGAATA
AGATTCTGGATTTGTGAGAATGAGAAAGGTGTTGCCCCCTGTAACATTTGGTTGCC
TATAAGCTGTATATCGTTGTGCTTGGTTGGCTATGTTCTATCTTCTCTTTACT
AATGATCAAAGTGAAGAGTACAGTGATCCTAGAGCTGCAGTCACAATGGATTGGTTCT
TTAAATTGCTGCAGCAATTGCAATTATTATTGGGCATTCTCATCCAGAAGGAACCTTT
ACAACTGTGTGGTTTATGTAGGCATGCCAGGTGCCTTTGTTCATCCTCATACAACAGT
CTTACTTATTGATTTGCACATTGAAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTA
GTTGCTATCGTCCTGTTCTTGTCACTACACTCATCCAGGCCAGTTGTTGAGAAAACAAGGC
GTTCATCAGTGTCAACATGCTCCTGCGTTGGTCTGTAAATG

FIGURE 46

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDQQVELGSMQ
VMNKTRRIMEQGGAHFINAFTTPMCCPSRSSILTGKYVHNHNTYNNENCSSPSWQAQHES
RTFAVYLNSTGYRTAFFGKYLNNEYNGSYVPPGWKEVGLLKNSRFYNYTLCRNGVKEHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWIMRYTGPMPKIHMЕFTNMLQRKRLQTILMSVDDSMETIYNMLVETGELDNT
YIVYTADHGHYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNEAGCLNPHTIVLNIDLAFTILD
AGLDIPADMDGKSILKLLDTERPVNRFRHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRACYILENDTVQCDLDLYKS
LQAWKDHLHIDHEIETLQNKKIKNLREVRGHLKKKRPEECDCCHKISYHTQHKGRKLKHRGSSL
HPFRKGQLQEKDVKWLIREQKRKKKLRLKLLKRLQNNNDTC SMPGLTCFTHDNQHQWQTAPFWTLG
PFCACTSANNNTYWCMTINETHNLFCEPATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTNMDLDGGSYEQYRQFQRRKWP EMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCA GTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCGGCTCCAGATGCTGGGCCTCTGGGAGCACAGGCC
TCGTGGGATGGATCACAGGTGCTGTCGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCCACC
TGCTTTCACGGACGGCAGGACTGTGACCTGGAGAGGAACCTACAGCTGCAAGGGGAAA
CCGAGTCCGCCGGGCCAGCCTGGCCCTTCCGGCGGGGCCACTGGGAATCTTCACC
ATCACCGTCA TCTGGCCACGTATCTCATGTGCCAATGTGGGCTCCACCACCAACCCAC
CCCCGCCACACCCCTCACCACTCCACCAACCAACCAACCCCCACGCCACATCCCCGCCA
CGCTCGTGAGGCTGCTGTCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTCCATGTGGAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGCTTGCCTCAGTCGATTTGCATGGCATGCCCACTGTACTATGGC
AGCAGAGAACATGGAGGAACACTGGGTCTGCACTGCTGAAGGGTTGGGAGTGGAGAGCAAGG
GTGCTCTTCGGGCTGGACAGCCGTCTGTGACAGTGACTCCAGTGAGCCCAAGAAATG
ACAAGCGTGTCTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGGCTCTGACCTCTC
ATCAGGCTGTCAGGCCCTGGGGGGAGGGCACTGGAGAGGCCCTGAGAATGTCTTTT
GGTTGGAGAAGGCAGTGTGAGGCTGCACAGTCATTCTGGTGCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFR
RRGHHLGIFFFFFFHHRHPGHVSHVPNVGLHHHHPRHTPHHLHHHHPRHHPRHAR

FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCA GTGTTGGGATCCAGAGCCATGT CGGACCTGCTA
 CTACTGGGCCTGATTGGGGCCTGACTCTTACTGCTGCTGACGCTGCTGGCCTTGC
 GTACTCAGGGCTACTGGCTGGGTGGAAGTGAGTGCTGGTCA CCCCCCATCCGAAACGTCA
 CTGTGCCCTACAAGTCCACATGGGCTATGGT GAGACTGGCGGCTTC ACTGAGAGC
 TGCAGCATCTCTCCAGCTCCGCTCCATCGCTCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCGTGGCAGCATCTGAGTGAGGTGAGGAATCGCCCTCC
 CTGAGCTCATCGACCTCTACCAGAAATTGGCTCAAGGTGTTCCCTCCGGCACCCAGC
 CATGTGGTGACAGCCACCTCCCCAACCAACCATCTGTCCATCTGGCTGGCTACCCGCC
 TGTCATCTGCCTGGACACCTACATCAAGGAGCGGAAGCTGTTGCCTATCTCGGCTGG
 AGATCTACCAAGGAAGACCAGATCCATTCTATGTGCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCCTGAGATGAAGGAGACAGAGTGGAAATGGGGGGCTTGTGGAGGCCATTGACACCC
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGTGCACACTGTCACTGGGGCAGCAGCCGTGGCTGGGAT
 GACGGTGCACACCCGAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGCTCTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGGCCCTAGGGAGTCACGGCTGGACCCCTGGACTGAGC
 CCCTGGGACTACCAAGTGGCTGGAGCCCCTGGCCACTGCCCTGAGAAGGGCAAGGGTAACC
 ATGGCCTGCACCCCTCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTTCCCTCTCTGGGGAGGGGGGTCCCTGAGGGACCTGACTTCCCTG
 TCCAGGCCCTTGCTAAGCCTCTCTCACTGCCCTTAGGCTCCAGGGCAAGGGAGCCA
 GGGACTATTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTTGTCTTTTCAGACTC
 ACAGTGGAGCTCCAGGACCCAGAATAAGCCAATGATTTACTTGTTCACCTGGAAAAAAA
 AAAAAAAA

DRAFT - 12/26/09

FIGURE 51

MSDLLLGLIGGLTLLLLLTLAFAAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTECSISPRLRSIAVYYDNPHMVPDKRCAGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPALAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESAGSSFEELDLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGGGGAAACGCTGCCTGGCTGCCGCCACCCGAACAGCCTGCCTGGTCCCCGGCTCCCT
GCCCGCGCCCAGTCATGACCCCTGCGCCCTCACTCCTCCGCTCATCTGCTGCTGCTGCT
GCTGCTCAGTGC GGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACC GAAAGTCCGTCGG
CCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCCAGCCGCTGCTTTGGA
GACACGCTTACATACACTACACGGGAAGCTGGTAGATGGACGTATTATGACACCTCCCT
GACCAGAGACCCCTGGTTATAGAACTTG GCCAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCGACATGTGTGGAGAGAAGCGAAGGGCAATCATCCTTCTCAC TTGGCTAT
GGAAAACGGGGATTTCCACCATCTGCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCA ACTACTGGCTAAAGCTGGTAAGGGCATTTCGCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCTGGGCTCATGGGTATCACCTATA CAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAACGAAACAAGAGCAAAAGAAATA
ATAAAATAAATTTAAAAAACTTAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLSSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCCGGGAACTGTTCCTGGCTGCCGCACCGAACAGCTGCTGGTCCCCGGCTCCCTGC
CCCCGGCAGTCATGACCCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGGCGGGTGTGCCGGCTGAGGCTGGGCTGAAACCGAAAGTCCGTCGGAC
CTCCAAGTGGAGACCTGGTGGAGCCCCAGAACCATGTGCCGAGCCGCTCTTTGGAGA
CACGCTTCACATACACTACAGGGAAAGCTGGTAGATGGACGTATTATGACACCTCCCTGA
CCAGAGACCTCTGGTTATAGAACCTGGCAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTTGGAGAGAACGGCAAGGGCAATCATTCTCACTTGGCTATGG
AAAACGGGATTTCCACCATGTCAGCGGATGCACTGGTGAGCTGAGCTGGAGCTGA
TTGCACTAATCCGAGCCAACACTGGCTAAAGCTGGTAAGGGCATTTGCCCTGGTAGGG
ATGGCCATGGTGCACCCCTCCTGGGCTCATGGGTATCACCTATAAGAAAGGCCAATAGA
CCCAAAAGTCTAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAGAAATAATA
ATAAATAAATTTAAAAACTTA

FIGURE 55

CCGAAAGTCCCCTCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTGGAGACACGCTTCACATACACTACACGGGAAGCTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACCTGGCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTGCACATGTGTGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCTATGAAAACGGGGATTTCCACCATCTGCCCCAGGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCGAGCCAACACTGGCTAAAGCTGGTAAGG
GCATTTGCCTCTGGTAGGGATGGCATGGTGCCAGCCCTCCTGGGCCTATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAATAATAATTTAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGCTGGAGGCTGTGGCCGTTTGTGCTGGCTAAAATCGGGGGAG
 TGAGGCAGGCCGGCAGCGACACCGGGCTCGGAACCACTGCACGACGGGCTGGACTG
 ACCTGAAAAAA**ATGT**CTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGG
 GAAAAGCGCAATACTATTGCTCCATTGCTGCTGGTGTACTATTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTATCCACCATGAAAGATTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCAGCCTCCATTGATTCAGTGCAGTATCGAATGGACAAGTCGGA
 GGTGATAGTTACAGTGAAGGGTGTCTGGTCAAACAGGTGCTCGCATTTGGCTTTCGTTGG
 TTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGTGGATTCTTTGGAGGTTATGTTG
 CTAAGAAAAAGACATAGTATAACCTGGAATTGCTGTATTTCAGAATGCCTCATCTT
 TTTGGAGGGCTGGTTTAAGTTGCCGCACTGAAGACTTATGGCAG**TGA**ACACATCTGAT
 TTCCCACAGCACACAGCCCTGCATGGTTGTTTTTACTGCTCACTCCAACCTT
 TTGTAATGCCATTCTAAACTTATTCTGAGTGTTAGTCTCAGCTTAAAGTTGTAACTT
 AAAATCACGAGAACACCTAAACAACACAAAAATCTATTGTGGTATGCACTTGATTAACCT
 ATAAAATGTTAGAGGAAACTTCACATGAATAATTGTCAAATTATCATGGTATAATT
 TGTAAGGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTGTCA
 TCTGAGGTCCAAAACCACAATGAAAGTCTGGAAGATTAAATGTGTTATTCAAATGTGGT
 CTCTTCTGTCAAATGTTAAATGAAATATAAACATTAGTTTAAATATTCCGTGG
 TCAAAATTCTCCCTCACTATAATTGTATTACTTTACCAAAATTCTGTGAACATGTAAT
 GTAACTGGTTTGAGGGTCTCCAGGGGTGAGTGGACGTGGAAAGAGAGAACCCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCTCCATGGGAAGGTCTCCGCTGCCCCCTCATT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCAC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDAAVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

FIGURE 58

TTCTTGGCTAAAATCGGGGAGTGAGGCAGGGCCGGCGCGCGCACACCGGGCTCCGGAAACC
ACTGCACGACGGGCTGGACTGACCTGAAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAACATGCATTGACTGGGGGAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTACAGGCTGGGATTATCATAGATGCAGCTGTTATTATCCCACCATGAAAGAT
TTCACCACTCATACCATGCCTGTGTTAGCAACCATAGCCTCTAATGATTAATGC
AGTATCGAACATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTGGCTTTCGTGGTTTCATGTTGGCCTTGATCTGATTGCATCTATGTGG
ATTCTTTGGAGGTTATGTTCTAAAGAAAAAGACATAGTACCCCTGAAATTGCTGTATT
TTTCCAGAACATGCCTTCATCTTTGGAGGGCTGGTTTAAGTTGGC

FIGURE 59

TGGACGGACCTGAAAAAAATGTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGAAAAGCGCAAATACTATTGCTTCATTGCTGCTGGTGTANTATTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTCACCANTCATACC
ATGCCCTGTGGTGTATAGCAACCATAAGCCTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGGCTCAAACAGGTGCTCGCATTTGGCTTT
CGTTGGTTCATGTTGGCCTTGGATCTGATTGCATCTATGTTGGATTCTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTGGAGGGCTGGTTTAAGTTGGCCCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTCCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAAATGTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTACAGGGTGGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGTCAAACAGGTGNTCGCATTTGGCTTTCGTTGGTTTGTGCTAAAGAAAAAGACATAGTAT
CTGATTGNATTCTATGCGGATTCTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCTGGAATTNCTNTATTTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGGTANTATTTTACAGGCTGGGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTNAACCANTCATACCATGCCGTGGTGTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGGCTTTNGTGGTTCATGTTGGCCTTGGATCTN
TGATTGCATTTATGTGGATTNTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTGTNTTGGCTAAAATCGGGGGAGTGAGGC GGCCGGCGCGG
CGNGACACCGGGTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAAATGTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCGTGCTGGTGTATAGCAACCA
TAGCCTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTCGTTGGTTCATGTTGGCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTGGAGGTTATGTTGCTAAAGAAAAGACATAG
TATACCCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTGAGGGCTG

FIGURE 63

CGACGGCCGGCTG**ATGTGGCTCCGCTGGTCTGCTCCCTGGCTGTGCTGCTGCTGGCCGTCC**
 TCTGCAAAGTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCCTTCTCCGAAGATGTC
 AAACGGCCCCCAGGCCCTGGTAACGTGACAAGGAGGCCAGGAAGAAGGTTCTCAACAAAGC
 TTTTCAGCCAACCAAGTGGCGAGAACGCTGGATGTGGTGTAAATTGGCAGTGCTTGGGG
 GCCTGGCTGAGCTGCAATTCTAGCTTAAGCTGGCAAGGGAGTCTGGTGTGGAACAAACAT
 ACCAAAGCAGGGGGCTGCTGTACACCTTGGAAAAGAATGCCCTGAATTGACACAGGAAT
 CCATTACATTGGCGTATGGAAGAGGCAGATTGGCAGTGGAGAGAAAGCTACATTAGGGCC
 AATGGCGAAAGGAGTACCCCATGTAACAGTGGAGAGAAAGCTACATTAGGGCC
 GAAGCTTCCACAGGAGGAATCATGTAAGCTGGATAAAAGCTGGTTAAGGTGTTATCCA
 GTGGACCCCTCATGCCATCTGTGAATTCTCCATTGGCCCTGGTCACTGGCTCTGAC
 AGGTGGCTGAGCTGCTGTTCTCTCTGAGCTCAGGCACTACTGCTACATCTTCCCA
 GGTCTGAGCAGCTGGGGCCCTCTGAGCTCAGGCACTACTGCTACATCTTCCCA
 CTTACGGTGTACCCCCAACACAGTGGCTTCTCATGCAAGGCTCTGGTCAACCAACTAC
 ATGAAAGGAGGTTTATCCTCCAGGGGGCTTCTGAAATTGCTTCCACACCCTCTGT
 GATTCAAGGGCTGGGGCTGTCTCACAAAGGCACACTGTGAGCTGGTCAAGACTGTGACT
 CAGCTGGAAAGGCTGTGGTCTGAGCTGTGAAGAAGGGGATGAGCTGGTGAACATCTATTG
 CCCATGTTGCTTCAACAGGACTCTCAACACCTATGACACACTACTGGGGGGAAACGC
 CCGCTGGCTGAGGCACTGGGGAGCTGGGGAGCTGGGGCTTAGGGCATGACCT
 CTGTTTCTCATCTGCTGGAGGACCAAGGAAGACCTGCACTGGCTGTCACCAACTACTAT
 GTTAACTATGACACGGACATGGACAGGAGCTGGAGGCGTACGCTCCATGGCCAGGGAAA
 GGCTGGGAACATTCCTCTCTCTCTGTTCTGCTTCCACATGACCAAAAGATCCGACCTGG
 AGGACCGATTCCAGGGCGTCCACATGATCATGCTCATACCAACTGCTACTGAGTGGTT
 GAGGACTGGCAAGGCTCTATGTCACTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGG
 AGAGTGTGACTGAGGATCCCCACTACCAAAACAGTCTATGCTGGCTGTCCTCCAGGGTGC
 TGCTACGGGGCTGACCATGACCTGGGGCCCTGCACCACTTGTGTGATGGCTCTTGG
 CCAGAGGCCCATCCCCAACCTATCTGACAGGGCAGGATATCTCACCTGTGACTGTGCTG
 GGGGCTGCAAGGTCGGCTCTGCAAGCCAGGCTCATCTGAAAGCGGAACTGTACTGAGC
 CTTAAGAATCTGATTCTAGGATCCGGGACAGAAGAAAAAGAA**TAG**TTCCATCGAGGGGG
 AGTCAGGAAATTGGCCAATGGCTGGGCACTCCTCTGACTTACCCATAATGTCCTTCTG
 CATTAGTCTCTGCACTGATAAGCACTCTAATTGTTCTGATGCCCTGAAGAGAGGGCTAG
 TTAAATCACAATTGGCAATGGGCAATGGAACACTGCTCTCCAGCTGGGGCAGGGTGGAGA
 TCTTACGGCTTTATAACATGCCATCCTACTAATAGGATAATTGACTTGGATAGCTTGTG
 TCTCATGACAGGGCCCTCTGCATCCCTACCCATGCTTCAACTCAGTGATCAAAGCGA
 ATATTCCACATCTGCTGATAGAACCCCTGGCAGTGTGTCAGCTCAACCTGGTGGGTTCA
 TGTCCTGAGGCTCTGCTCTCATTCATTAGTGTCACTGGCTGCAAGTTCTACACTGTCAAGG
 GAAAAGGGAGACTATGAGGCTTAACCTCAAAACCTGGGCTGGTTTGGTTCCTGCA
 GGTTGGAGAGCTAGATCTCTTGTCTGGGCTCAGTGGCTCTCAGGGGACAGGAAT
 GCCTGTTGAGCTGGGAGCTGTGGGAGCTGGGTAACAGCAGGATCCTCAGTTAGTA
 GGGTGCATGTCAGATGATCATTCACATTGATGGAGCTGGGAGCTGAGCTTGTGAGGCT
 TCGGGGTGGCAGCTGGTCTCAATGTGCCAGCAGGAGACTCAGTACCTGAGGCTCAATCAAGC
 CTTATCCACAAATACAGGGAGGGTGTGAGGGAGGGTACATCAGGAGTCAAGGCT
 TGGACTGGTAAGATGAAACTTGTCTGGCTGAAGCAGGCTGCAAGGGCATTCCAGGCAAGGG
 CACAGCAGGGGACACTGCAAGGGAGGTGTGGGGTAAGGGAGGGAGTCAACATGAGG
 AAGCCACGGAAATGTGTGTAAGCCAGAAATGGCATTTGAGCTTAATTAGCACATGTGAGGG
 TTAGACAGGTAGGTGAATGCAAGCTCAAGGGTTGGAAAATGACTTTTCAGTTATGTTG
 GTATCAGACATACGAAAGGTCTTGTAGTTCGTGTTAATGTAACATTAATAAATTATTG
 ATTCCATTGCTTAAAAAAAAAAAAAA

FIGURE 64

MWLPVLVLLAVLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAFLVTDKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPO
EEAIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTKATVQSVLDSAGKACGVSVKKGHELVNJIYCPIVVSAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGKTEDLHLPSTNYYVYYDTDMQAMERYVSMMPREEAAEH
IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEEWQAEKGKRGSDYETFKNSFVEA
SMSVVLKLFPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

FIGURE 65

GCAGCGCGGAGGGCGGCGTGGCTGGCTGAGTCGGTGGTGGCAGAGGCCAAGGCCACAGCTCTA
 GGGGTTGGCACCGCCCCGAGAGGAGG**ATGCGGGTCCGGATAGGGCTGACGCTGCTGCTGTG**
 TCGGGTGCCTGAGCTTGAGCTGGCCTCGCGTCCTCGGATGAAGAAGGCAGCCAGGGATGAATCCT
 TAGATTCCAAGACTACTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATTTCTGATTCAAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACGCCCTAACAGGCCAACAGGGGAAAGTGTACAGAACAGATATCAGCTTCTAG
 AGTCTCAAATCCAGAAAACAAGGACTATGAAGAGCCAAGAACAGTACGGAAACCAGCTTTG
 ACCGCCATTGAAGGCACAGCACATGGGAGCCCTGCCACTTCCCTTTCTTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAAAGCAGATGAAAAGTGGGCTTTGTGAAACTGAAAGAGGCTGCTAACAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA
 TAAGAAAAGCaaaaAGAGAAGCATATCGTATCCTAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTCAATGCTTTTATTGGTGAATTACTTGCCACAGAACATAC
 CAGGCAGCGAGAGAGATGTTGAGAGCTGACTGAGGAAGGCTCCCAAGGGACAGACTGC
 TCTTGGCTTCTGTATGCCTCTGGACTTGGTGTAAATTCAAGTCAGGCAAAGGCCTTGTAT
 ATTATACATTGGAGCTTGGGGCAATCTAATAGCCCACATGGTTTGGTAAGTAGACTT
TAGTGGAAAGGCTAATAATTTAACATCAGAAGAATTGGTTTATAGCGGCCACAACCTTT
 TCAGCTTCATGATCCAGATTGCTGTATTAAGACCAAAATTCAAGTCAGTTGAACCTCCTCAA
 ATTCTTGTAAATGGATATAACACATGGAATCTACATGTAATGAAAAGTGGTGGAGTCCACA
 ATTTTCTTAAATGATTAGTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAATGGC
 TCTTTTAAATTTCTGTAGTTGCAAAATTGTAATGGTGTATAGAAAACACAT
 GAAATATTACAAATTGGCAACAAATGCCCTAAGAATTGTTAAAATTGAGTTATT
 GTGCAGAATGACTCCAGAGAGCTCTACTTCTGTTTTACTTTCATGATTGGCTGCTTC
 CCATTATTCTGGTCATTTATTGCTAGTGCACACTGTCCTGCTCCAGTAGTCATTTCC
 CTATTTGCTAATTGTTACTTTCTTGCTAATTGGAAGATTAACTCATTTAAATAAA
 ATTATGTCAGATTAaa
 Aaa

1000 1000 1000 1000 1000 1000 1000 1000 1000 1000

FIGURE 66

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLDSKTTLTSDESVKDHTTAGRVVAGQIFLD
SEESELESSIQEEEDSLKSQEGERVTEDISFLESPNPENKDYEERPKKVRKPALTIAEGTAHG
EPCHFPFLFLDKEYDECTS DGDREDGRLWCATTYDYKADEKWGFCETEEEAAKRQRQMQEAEEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLQPQNIQAAREMFKEK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIAHMVLVSRL

FIGURE 67

CTTCCCAGCCCTGTGCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCTT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCCTAGCTTCCTCTGATGGGACCTTCCT
GTCAGTTCCCAGACAGCTCTGCCAGCTGGATGCACGTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGGCTCAGCCCCCAGCACGTACCGATCAGGGACTACGGTGTGCTTGG
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGCAGCCAAGGGATGAGGCCACAATGCCT
GTGTCCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTAGTCCC**TAG**GGGTGGGTGTGAGATGGGTGCCTCCCTCTGCTCCCATTTCT
GCCCTGACCTTGGTCCCTTTAAACTTCTGTGAGCCTGCTCCCTGTAAAATGGG
TTAATAATATTCAACATGTCAACAAAC

68/330

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYYCSVGYGFSP

FIGURE 69

FIGURE 70

MTPSPLLLLLPPLLGAFPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVVCKATNGFGSLSVNYTLVLDIISPGK
ESLGPDSSGGQQEDPASQQWARPRFTQPSKMRRVIARPVGSSVLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKWTLSLNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKVIQWLKRVEYGAEGRHNSTIDVGGQKFVLPTGD
VWSRPDGSYLNKLITRARQDAGMYICLGANTMGYSFRSAFLTVLPDPKPPGPPVASSSSA
TSLPWPVIGIPAGAVFILGTLLWLCAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPs
LAALSAGPGVGLCEEHGSPAAPQHLLGP GPVAGPKLYPKLYTDIHTHTHSHTHSHVEGKV
HQHIHYQC

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FIGURE 71

FIGURE 72

MVGTKAWVFSFLVLEVTSQLGRQTMLTQS VRRVQPGKKNPSI FAKP ADTLES PG EWTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGS PREGFWCLNREQ
 RPGQNCSNYTVRLCPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAIIYLLTK
 TPKLLTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAAТИKAЕFVRAEPTY
 MVMNPETKARRAGQSVSLCCATGKPRPDKYFWYHNDTLLDPMSLYKHESKLVLRKLQQHQAG
 EYFCKAQSDAGAVKSVAQQLIVTASDETPCNPVPESYLIRLPHDCFQNAFTNSFYDVGRCPV
 KTCAGQQDNGIRCRDAVQNCCGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVGRV
 SAADNGEPMRFGHVYMGNSRVSMTGYKGTFTLHV P QDTERLVLTFVDRLQKFVNNTKVLPFN
 KKGSAVFHEIKMLRRKEPITLEAMETNI I PLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
 KASVTFLDPRNISTATAAQD LNF INDEGDTFPLRTYGMFSVDFRDEVTESEPLNAGKVVKHL
 DSTQVKMPEHISTVKLWSLN PDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYR SERFPLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFD SVITGPNGA
 CVPAFCDDQSPDAY SAYV LASLAGEELQAVESSPKFNPNAIGVQPYLNKLNYRRTDHEDPR
 VKKTAFQISMAKPRFNSAEEESNGPIYAFENLRACEEAPPSSAHFRFYQIEGDRYD YNTVPFN
 EDDPM SWTEDYLA WWP KPM EFRACYIKVKIVGPLEVNVR SRNMGGTHRR TVGKLYGIRDVRS
 TRDRDQP NVSAACLEFKCSGMLYDQDRVDRTLKVPI PQGSCRRASVN PMLHEYLVNHLPLAV
 NNDTSEYTM LAPLDPLGH NYGIYTVDQDPRTAKEIALGRCFDGTS DGSSRIMKS NVGVALT
 FNCVERQVGRQSAFQYI LQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFP RVA
 QQPLIN

104777-13526660

FIGURE 73

CTGCAAGTTGTTAACGCCAACACACAAGTATGTTAGGCTTCACCAAAGTCTCAATAACCTGAATACCGCAC
 AATATCTTAACCTCTCATATTGGTTGGATCTGCTTGAGGTCCCATCTTCATTTAAAAAATACAGAG
 ACCTACCTTACCCGCTACGGCATACATACATATGTTATATATGTTAAACTAGACAAAGATCCAGACATCATAAAAGC
 AAAGCTGCTTAGTTCCAAGAAGATTACAAAGAATTAGAGATGATTGTCAGATCTGCTTCTGATTCTG
 CCCCCTTGGGTTACGGTGTCTCAGTGTGAGCAGGCCCTACCCCTGGTTGGGACATTATGATTGTCAGAAGACT
 CAGATTACCGGAAGAAGGGAAAGTTGGGATTACATGGCTGCCAGCGGATCACCGGACATGACAAAATA
 TCTGAAAGTGAACACTCGATCTCCGGATATTACCTGTGGAGACCTCTCGAGACGTTCTGCAATGGGCAATC
 CCTACATGTCATAATAGTGTGAGCTGGAGCACACCCCCCTGAGCTGATGTTGATTIT
 GAGGAAGACATCTCCACATTGGCACTCTGCCACTTGGAGGATATCCAAGCCTCTCAGGTTAACAT
 CACTCTGCTTGGAGACATTGAGCTAACAGACAACTAGTTTACCTTGAATCTGGGCTCAGACGACC
 AAATGATCTTGGAGACAGTCTCGATTAAGGACAACTGGCCCTATCAGTATTATGCCACAGACTCTTA
 GATGCTTTCACATGGATCTAATCCGTGAGGATTATCACAGCATACTGGCTTGAATACAGGTTGGGCTT
 AGAGTACTAACAGGGTATACAAACARTACAAACATTACACTTGAATACAGACAGGTTGGGCTT
 CTGGACCTCTGGCTACCCAAATGGCTTCTACGGGACAGCTGGATACACCCAGAAACTCAGAGATTCTT
 ACAGTCAGACAGGCTTGGAGGTTGTAAGACAGCCGTTGGGAACATCTGGCTGAGCTACACTGGC
 ACGGCTACTTCTACGGCATCTGACATTAAGGCTGGAGGAGGTGCAACTGTATCTCCATGCCACTGTATG
 TGTTATGCAACAGCAAATTGACATGCCATGTGAGCACACACTACAGGTGCAAGCTGTGGGAATGCAAGA
 AATTATCAGGGCGGACCTTGGAGTCAGGCTCTCTCCACCCCAAGGGCACTGCAAAATACCTGTATCCC
 CAGATTTCAGTATTGGTACGATGTCTGCACACAAGCAGCTCTGCACTGCCAGAACGGGGACCTGGCACA
 ACAACCTGGGCTGGCTGTCGGCCGGCGCATACCGGCATCTCTCGAGAACGTTGGGCTGCGAGGAGGCTGG
 AGCTCGGGCTCGGACTCTGGCAGGGCGGGCCCGACGGCACCCACGGCTGCTGCTGACCGCTGCT
 GGGAACGCCAGCCCTGGTGTGTCAGGTGCACTTCCAGGACACCCAGGACGGGCGCTGCGCTGGGAAGGC
 GACACACCCAAACTATTGCTACTAACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCAACTGTGACTAAAGGCTATTATCACCGTGGACAGCACATCGAGTCAAGACTGTAAATTTC
 TGAACCTGAGGAGTTGGCAGCTGTGATATTACTGCAACATTCAGTGGCAGCTGGAGACATTTGTG
 TTGGAAAGGCTGGCAGCCGGCCAAACAGGAAAGACAAAACAACAAATCAACCGACCTAAACATATTG
 TACTCTAGCGTGTGGCCTAGTACGACTCCGGCCAGTGTGGGACCAACAAATAGCATTCTTGTCTG
 GTGCGATTGTGGCAATAGGAAATTCTGTTAACAGCTGCAATTGGCTGCTTCCGTCTGAAATCCCTTCAAC
 CTGTGCTTATTGTAACGTTGCTCTGTAACCTCGTTGGTGGAAAGATTCTTGTCTGATGTTAGTGTGATGCCA
 TGTTGTAACAGCCCTCTAAAAGGCCAACGGCAGTACATCCCTGTATATCTTACGAGCAGTGGCTGCGA
 GCACACACCCACTAACAGAAGTGGCTATTAGGAAAAGAAGTGTATCTCTTGTATTCAAAATGAAGIT
 ATTTCCTTGAACTACTGTATATGTTAGATTTTTGTATTATGCAACATGGCAATTGGTGTACAGACAACTGTGTTAAT
 GTATCTAATTGCAATCAGGAAAGACTGACATTATTGCTCTTCTCTTGTGTTTGTCTACTGTGCA
 GATTCTCTGTAAGGGCAACGAAACGTGCTGGCATCAAAGAATATCAGTTAACATATAACAAACTGTAAAGA
 TTCCACAAAGGACATTCTTAATGTTCTGTGCTTAAACACTGGAAAGATTAAAGATAAAAACACTCTGCA
 TAAACGATTCAAGGAATTGTATGCAATTCTTAAGATGAAGGAAACGCCAACAGCAGTTACACTCA
 TTACTGATTCTGTGTGACTGAGTACATTGAGCTGACGAAATTGTTCCAGGAAAGATGGATTGATGTTACT
 AGCTGGACAACTTCTGCAAAATATGAGACTATTTCGACTTGGAAAATTACAAACAGCBBBBBBBBBBB
 AAAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMDTKYLN
VKLDPPDITCGDPPETFCAMGNPYMCNNEDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVTFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLIRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDGKCKNYQGRPWSPGSYLEIPKGTTANTCIPSISIIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLREEAGSCGSDSGQGAPPHGTPALLLTLGTA
PLVF

FIGURE 75

CCCACCGCGTCCCCGTGACCTGGGCCAGCCCTCCCGTCGGCTAAGATTGCTGAGGAGGCCG
 CGGGTAGCTGGCAGGCAGCGACTTCAAGGCCCGTCCGGCGAGGTGTCCTCATGACTT
 CTCTTGCGACC**ATG**TCCGTATCTTTGCCTCGTGGTACGGTAAGGGATGGACTGCC
 CCTCTCAGCCTACTGATTTTACACACCCAAGATTTTGAATGGAGGAGACGGCTCA
 AGAGTTAGCCTTGCAGTGGCCAGTATCCAGGTCAGGTTCTGCAGAAGGTTGTACTT
 AGTATAACATTTCTTCTTGCAGTGGCTCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTCTGCTTCTGGAGACCCCTGTGGTGGAAATTCACAGCTTCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTCTGAGTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTAACTATGTAAGTTCTCTCAGATGGAGTGCAGCTGGAAAAAA
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGTGATGAATGGTACACACCCGATGCACTGGAGCCTGCTCTAATTCGAATGGAA
 CCAGTGACAGCCCTGGGTATCTCTCCCTCATTCTAACATCATGTTGCTGCCCTGAATCT
 CATTGAGGAGTTCACCTTGAGAACATTCTTACAGGATCCAAGGGAGCTGGTTCTGCTGGT
 TGGACCAAAACCTCG**TGA**CCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CGGGAGCAGTGTCAAACCTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGGCATGTCAGTGAATCTGGGAATGGCTGGATTGGAAACATCTGCCCATGTTGATTG
 ATGGCAGAGCTGTTGCCACAAGGCCCTTATTAGGGTAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGTTAGTACATATGACCTTAAACCTTACATTATATGATTCTGGGGTT
 GCTTCAGAAGTGTATTTCATGAATCATTGATTTGATCCCCAGGATTCTATTTGT
 TTAATGGCTTTCTACTAAAGCATAAAATACTGAGGCTGATTAGTCAGGGCAAAACCAT
 TTACTTACATATTGCTTTCAATACCTGCTGTTCATGTTACACAAGCTTCTAGGTTTTC
 TTGTAACAATAAATATTGAGTAAATAATGGGTACATTAAACAAACTCAGTAGTACAACC
 TAAACTGTATAAAAGTGTGTAAAATGTATAGCCTTATATCCTATGTATAAATTAAATG
 AGGTGGCTTCAGAAATGGCAGAATAATCTAAAGTGTATTAAAAAAAAAAAAAAAAAAAA
 AAAAG

FIGURE 76

MSVIFFACVVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMFPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDDQTS

FIGURE 77

TGCTT CCTGGAGACCC TGTGGTGGGAATT CACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTCTTGAGTTGACAGCATCATT CAGAAAGTGAAGTGGCATT
TTAACTATGTAAGT CCTNTCAGATGGAGTGCAGCTTGGAAAAAATT CAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGTT

FIGURE 78

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGGGGTGTTGCATTGAAACGTGAGCGGA
 CCCGACCTTAAAGAGGGGAGCAAAGGGAGGACAGAGCCCTTAAACGAGGGGGTGGTG
 CCTGCCCTTAAGGGCGGGCGTCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGGCTGGTCTGGGTGCTTGGCGGGCGGCTT
 CCTCCCCCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGTATCCGTGCGAGAACAGTATTCCAGCAGAGGATCCGC
 GAGTGTTTATATCAACACTCTGTGTTGCAACACTGTACATCCTGCCACATCTCTGAC
 CCGCTTCAAGAAGGCTGCTGAGTTCACACAGTGGATGAGATGCCACCGTCAAAAGA
 TTGCGCTGAGCTGTCACCTTACCCCTGCAATTGCGCTGGTGTCTGCTCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACATACTACATCCAGTGGT
 CAACAGCCTCCATCATGAGGCTCTGGAAACCTTCTTCTCTCCCAACTGTCCCTCA
 TCTTCTCATGCCCCCTGTCATATTCTACTGAGCTGAGGCTTGTGCTGCTGAGAAAG
 GGTGCTGGGCGGTCTATGAGACAGTGGTGTGATGTTGATCTCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGTGCATCAGGCCATTGGAACAGAACAGGCAACAGAGACTCT
 ATGACTTTGGAGTACTATCTCCCTACCTCTACTCATGCACTCTCTTGGGGTCTG
 CTGCTCTGGTGTACTCCATGGGCTCGCCCGCATGTTCTCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTGAGGAG
 CAGCCCTGACCGCAGGATCTGAATCTACTCTGCTGGCTGCCCTTAGACATGGAGCTG
 CTACACAGACAGGCTGGCTCGACACAGACAGGGCTCTGCTGGAGAACAGGGCAAGGC
 TTCAGCTTGGCAACGGAACCTGGCTACCCCTGGCTATGCTGTGCTGGTGTGACGG
 GCCTGTCTGTGCTCATGTGGCATCCACATCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCGAGGCTGAGGGTACCTCTAGGGCTCTTCTCAAGCTGGGCTCTTGG
 TGCGCTATCAGGTTGACTCATCTTACCTAATGTTGCTCTCAGTTGTTGGCTTCTATA
 GCTCTCACTCTTCCGGAGCCCTGGGCCAGATGGCACGACACTGCCATGACGCCAGATAATT
 GGGAACTGTGCTCTCTGGCTTAAGCTCAGCACCTCTCTCTGCAACCCCTGGG
 GCTCACTGCTTGGCTGCTGGTGAATTGGACGCTTCACTGGCTGGCAATTCTACA
 TTGTGTTCTCTACAACGCGAGCCTTGCAAGGCTCACACACTCTGCTGGTGAAGACCTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCTTGGGCTGGACAGACTGCCGTGCCGT
 CTCCGGTTTCCCCAGGCACTAGGAAGACCCAGCAGCAGACTGGCTTGGGGTGGGA
 AGGAAAAAACTGGACACTGCCATCTGCTGCTAGGCTGGAGGGAGGCCAACGGCTACTTGG
 ACCTCAGGACCTGGAACTTGAGAGGGTGGGGTGGCAGAGGGGAGGAGAGCCATCTGCACTATT
 GCATAATCTGAGCCAGAGTTGGGACCCAGGACCTCTGCTTCCATACCTTAACCTGTC
 CAGCATGGGTAGGGCTGGGTGACTGGGCTAGCCCCTGATCCAAATCTGTTACACATCA
 ATCTGCTCACTGCTGTTCTGGGCATCCCATAGCCATGTTACATGATTGATGTGCAAT
 AGGGTGGGTAGGGCAGGAAAGGACTGGGCCAGGGCAGGCTGGGAGAGATAGATTGCTCC
 CTTGCTCTGGCCCAGCAGAGCCTAAGCACTGTGCTATCTGGAGGGCTTGGACCCACCTG
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTCAGCCATCAGCAATAAGTTGATCCAGGG
 AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCFTLAIALGAVLLLPSIISNEVLLSLPRNYYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFGASRKGVLRVYETVVMLMLTLLVLMVVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPPTSCWLPLDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMSSVVGFY
SSPLFRSLRPRWHDTAMTQIIGNCVCLVLSSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
IVFLYNAAFAGLTTLCLVKTFAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

FIGURE 80

GGCTGCCGAGGGAAAGCCCCCTTGGTTGGTCTTGGTTGCTTGGCGGCGGCNNNTCCNTCCCC
GCTCGTCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCAGTGTA
TTATATCAACACTTCTGTTGCAACACTGTACATCCCTGCCACATCTTCCGTACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTAAAACGAGGC GGTTGGTGC
CTGCCCTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGTCTGGTCTGGCGGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCCAGT
GTATTATATCAACACTCTGTTGCAACACTGTACATCNTCTGCCACATCTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTACCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCGCCCTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCAAACCTGTTT
GGAATTGAGGAAACTTCTCTTTGATCTCAGCCCTGGTGGTCCAGGTCTTCATGCTGCTGT
GGGTGATATTACTGGTCTGGCTCTGTCACTGGACAGTTGCAAGGACACCCAGGCCATT
ATTTTCCCTCCAGCCTCATGGACCACAGTCTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTCGCTTCACTCACACAGAAAACAAAATGGTACCATCGGTACCTTGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTAGGAATCTGGAGAGTACAGATGCCAG
GCCAGGGCTCCCTCTAGTAGCCCTGTGCACTGGATTTCTCAGAGATGGGATTCC
TCATGCTGCCCAAGGCTAACATGTTGAACCTGGCTCAAGTGATCTGCTCACCTAGGCCTCTC
AAAGCGCTGGGATTACAGCTCGCTGATCCTGCAAGCTCCACTTCTGTGTTGAAGGAGAC
TCTGTGGTCTGAGGTGCCGGCAAAGGCGGAAGTAAACACTGAATAACTATTACAAGAA
TGATAATGTCCTGGATTCTTAATAAAAGAACTGACTTCAAAAAAAAAAAAAAAA
AAA

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAQANVELLGSSDLT

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTCGGGACCAGGGAGACCCCCGCGCCCCCCCCTGAG
 GAGGCGGCCTCACAGGGCCGGTGGCTGGCGAGCCGACGCCGGCGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGACAGAGGAACC**ATG**GCTCCGAGAACCTGAGCACCTTGC
 GCCTGTTGCTGCTATAACCTCATCGGGCGGTGATTGCCGGACGAGATTCTATAAGATCTTG
 GGGGTGCTCGAAGTGCCTCTATAAAGGATATTAAAAGGCCTATAGGAAACTAGCCTGCA
 GCCTCATCCGACCGAACCCCTGATGATCCACAAGCCCAGGAGAAAATTCCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTAGATAGTGGAAACAGGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGATGGTCATCAGAGCTCCATGGAGACATTTCACACTCTTGGGATT
 TGGTTTCATGTTGGAGGAACCCCTCGTCAGCAAGACAGAAATTCCAAGAGGAAGTGTGATA
 TTATTGTAGATCTAGAAGTCATTTGAAGAAGTATATGCAGGAATTGGAGAGATTTGTTGGAAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCTGGCAAACGGAAAGTCAATTGTGGCAAGAGAT
 CGGGACCAACCCAGCTGGGCCCTGGCGCTTCAAATGACCCAGGAGGTGGTCTGGACGAAT
 GCCCTAATGTCAAACTAGTGAATGAAGAACGAAACGCTGGAAAGTAGAAATTAGACCTGGGTG
 AGAGACGGCATGGAGTACCCCTTATTGGAGAAGGTGAGCCTCACGTGGATGGGAGCCTGG
 AGATTTACGGTTCGAATCAAAGTTGTCAAGCACCAATTGGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCAGTGGTTGGCTTGAGATGGATAATTACT
 CACTTGGATGGTCACAAGGTACATATTCCCGGATAAGATCACCCAGGCCAGGAGCAGAAGCT
 ATGGAAGAAAGGGAAAGGGCTCCCAACTTGACAACAACAATTCAAGGGCTTTGATAA
 TCACTTTGATGTGGATTTCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAA
 CAGCTACTGAAACAAGGGTCACTGCAGAAGGTACAATGGACTCAAGGATAT**TGA**AGGTG
 AATAAAATTGGACTTTGTTAAAATAAGTGAATAAGCGATATTATTATCTGCAAGGTTTT
 TTGTTGTTGTTTGTGTTTATTTCAATATGCAAGTTAGGCTTAATTGGGTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTGTCATTGCACTCGGAAAGAATGACC
 AGCAAAAGGTTACTAATACCTCTCCCTTGGGATTTAATGTCGGTGCTGCCGCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGAAAAGAAACACAATTAGAGGGTTGGA
 GTTGTAGCAATTCAAAATGCCACTGGAGAAGTCTGTTTAAATACATTGTT
 TTATTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLAQLHPDRNPDDPQ
 AQEKFQDLGAAYEVLSDSEKRKQYDTYGEEGLKDGHQSSHGDI FSHFFGDFGMFGGT PRQQ
 DRNIPRGSDIIVDLEVTVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
 MTQEVCDECNPVNKLVNEERTLEVEIEPGVRDGMEYPFFIGEGERPHVGDGE PGDLRFRIKVVKH
 PIFERRGDDLYTNVTISLVESELVGFMEDITHLDGHKVHISRDKITRPGAKLWKGEGLPNFD
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGAACCCGGGCCCCCGGTGGAGNGCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGCGGAGGAGGTTTGAGGATTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTGCCTGTTGNTATACTTCATCGGGCGGTGATTGCCGG
ACGAGATTNTATAAGATTTGGGTGCCTNGAAGTGCCTNTATAAGGATATTAAGGAG
CCTATAGAAACTAGCCCTGCAGNTTATCCGACCGAACCTGATGATCCACAAGCCCAG
GAGAAATCCAGGATTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGAAACA
GTACGATAATTATGGTAAGAAGGATTAAGATGGTNATCAGAGCTCCATGGAGACATT
TTTCACACTNTTGGGATTTGGTTCATGTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGAGGGCGGGGGCAGTCGGGGATGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGCGGGAGGAACCTAGCACCTGCATCCTCTTCCCAATTGCCACTTCCA
 GCAGCTTAGCCCAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTGGAAGC**ATGG**
 AGACTGTGGTATTGGCCATAGGTGTGCTGGCCACCCTTTCTGGCTTCGTTGCAGGC
 TTGGTGCTGGTTGCAGGCAGCGCTACTGCCGGCCGAGACCTGCTGCAGCGCTATGATT
 TAAGCCCATTGTGGACCTCATGGTGCATGGAGACCCAGTGTGAGCCCTCTGAGTTAAC
 TGGACGATGCTGTATACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCTGCATTGCATCTGAAGATTGTCACACTCTGAC
 AGAGAAAGCTTGTGCATGACAATGGGCTCTGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCCTCGTGGACCCAAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCA
 TCACCTGGTGTGGTACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC
 AGTCTCTGTCGGCTGCTGAGGAGCATTTGGAAGTCCTCGAGAACGAGCCCTAGCTTCTGAG
 CCAGATAAAAGGCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATT**TAGTGCCT**
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCATCCCTGGATGGCTCAGCTTGCCTT
 CTACTTTCTATAGAGTTAGTTCTCCACGGCTGGAGAGTCAGCTGTGTGCATAG
 TAAAGCAGGAGATCCCGTCAGTTATGCCTCTTGCAGTTGCAAAACTGTGGCTGGTGAGT
 GGCAGTCTAACTACAGTTAGGGAGATGCCATTCACTCTGCAAGAGGGAGTATTGAAAA
 CTGGTGGACTGTCAGTTATTTAGTCACCTAGTGTTCAGAAAATTGAGGCCACCGTCT
 AAGAAATCAAGAGGTTACATTAATAGAATTCTGGCCTCTCGATCGTCAGAAT
 TGTGGCAATTCTGATGCTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTGGCAAGACTGTACTCTCACCCTGGCTGTTCAATTATTTGATTATCTGCCT
 GGTCCCTGAGCGCTCTGGTCTCCTCTCCCTTGAGGTTGGTTGAAGCTGAGGAAC
 ACAAAAGTTGATGATTCTTTTATCTTATGCCCTGAATTACCTAGCTACCACTAGGTG
 GATAGTAAATTATACTTATGTTCCCTCAAAAAAAAAAAAAAA

FIGURE 88

METVVIVAVGVLATIFLASFAALVLVCRQRYCPRDQLLQRYDSKPIVDLIGAMETOSEPS
ELDDVVITNPHEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTAS
VSDIIVVAKRISPRVDDVVKSMPPLDPKLLDARTTALLSVSHLVTRNACHLTGGLDWI
DQSLSAAEEHLEVLREAALASEPDKGGLPGPEGFLQEQAII

FIGURE 89

GCTTCATTCCTCCGACTCAGCTTCCCACCCCTGGGCTTCCGAGGTGCTTCGCCGCTGTCC
CCACCAC TG CAG CC **ATG** AT CT CCT TA AC GG AC AC GG CAG AAA ATT GG AAT GGG AT TA AC AG GA
TTGGAGTGTTTCTGTCTTGAATGATTCTTTTGACAAGCACTACTGGCTAT
TGGAAATGTTTATTTGATGCCGGCTTGGCTTTGTAATTGGTTAGAAAGAACATTGAGAT
TCTTCTTCCAAAACATAAAATGAAAGCTACAGGTTTTCTGGGTGCTGTTAGTC
CTTATTGGTTGGCCTTGATAGGCATGATCTCGAAATTATGGATTCTTCTGTTCA
GGGCTCTTCCGTGGCTTATTAGAAGAGTGCCAGTCCTGGATCCCTCTAAAT
TTACCTGGAATTAGATCATTTGAGATAAAGTTGGAGAAAGCAACAATATGGTA**TA**ACAACA
AGTGAATTGAGACTCATTTAAATATTGTTATTATAAGTCATTGAGAAATATTCA
GCACAAAATTAAATTACATGAAATAGCTGTAATGTTCTTACAGGAGTTAAACGTATAG
CCTACAAAGTACCAAGCAGCAAATTAGCAAAGAACAGCAGTGAAACAGGCTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAATGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTGAGGCTATTGTTGTTCCACAATGTGCGAAACTCAGCCATCCTAGAGAA
CTGTGGTGCCTGTTCTTTCTTTATTGAAAGGCTCAGGACATCCATAGCATTGCT
TTTAGAAGTGTCCACTGCAATGGAAAAATATTCCAGTTGCACGTATCTGGAAAGTGA
TGCATGAATTGATTGGATTGTGTCAATTAAAGTATTAAACCAAGGAAACCCAAATTG
ATGTATGGATTACTTTTTNGNCAGGGCC

FIGURE 90

MISLTDQKIGMGLTGFVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLRGFFPVVVGFIIRVPVLGSLLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

REF ID: T252663

FIGURE 91

GAAGACGTGGCGGCTCTGCCCTGGGCTGTTCCCGCTTCATTCTCCGACTCAGCTTCCC
ACCNTGGCTTCCGAGGTGCTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTCCTGTTGGAA
ATGATTCTCTTTTGACAAAGCACTACTGGCTATTGAAATGTTATTGTAGCCGGCTT
GGCTTTGTAATTGGTTAGAAAGAACATTCAAGATCTTCTTCAAAACATAAAATGAAAG
CTACAGGTTTTCTGGGTGGTGTATTGTAGTCCTATTGGTTGGCCTTGATAGGCATG
ATCTTCGAAATTATGGATTTCTCTGTTC

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTCTGGTTCTAAGTCATGTGCCAA
GGCTGCCAGGAAGGAGACGCCCTCCTGAGTCTGGATCTTCTCCCTTGAAATCTTGA
CTGTGGTAGTTATTCTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGACTG
TGAAGTCTCAGTCTGTGCCACCTGGTCTCTGTCAGTCCTTATTGCCCTCAGGCTAATC
ATCAACACCATTCACTCTTCACTCTCCCTCTGGCCATTAAACAAGCAGCTTCCGGAA
GATCAACTGCGAGACTGCTTATTGCATCTCAAGCCAGCTGGTGTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTCACGGACCCCGCGCCTACCTCAAGTATGGAAAGGAAAAT
GCCATCGTGGTCTCAACCACAAGTTGAATTGACTTCTGTGTGGCTGGAGGCCGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCAAGGCTCTGGCCAAGAAAGAGCTGGCCTATGTCCTAA
TTATCGGCTGGATGGTACTCACCAGATGGTCTTCTGTGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTGCAGCACCTCCGGACTACCCGAGAAGTATTTTCTC
GATTCACTGTGAGGGCACCGGTCACGGGAAAGAACATGAGATCAGCATGCAGGGCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGCTTCGCAC
ACCGTGAGGAGCTTGAGAAATGAGTTCTAGCTGTATATGACTGTACACTCAATTTCAGAAA
TAATGAAAATCCAACACTGCTGGGAGTCTAAACGGAAAGAAATACCATGCAGATTGTATG
TTAGGAGGATCCCACGTGGAAAGACATCCCTGAAGACGATGACGACTGCTGGCCTGGCTGCAC
AAGCTCTACCAAGGAGAAGGATGCTTCTAGGAGGAGTACTACAGGACGGGCACCTCCAGA
GACGCCCATGGTGCCCCCGGGCCCTGGACCCCTGTGAAGTGGCTTTGGCCTCGC
TGGTGTCTACCCCTTCTCCAGTTCTGTGTCAGCATGATCAGGAGCGGGCTTCCCTGACG
CTGGCCAGCTCATCTCGTCTTGTGGCTCCGGAGTTGATGGATGATTGGT
GACGGAAATTGACAAGGGCTGCTCACGGAACTCTGACAGCAAGCAGAAACTGAATGACT
GACTCAGGGAGGTGTCACCATCGAAGGGAACTTGGGAACTGGTGGCCTGCAATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGTGAGCCCTGCTGGCACGGCGAAGTCACGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGATGGGAGGAAGATGTTTGTAACTT
TTTCCCCATGTGCTTGTGGCTTGGTTCTTTGTGCGAGTGTGTGAGAATGGC
TGTGTGGTGTGGTGAACCTTGTGTCAGATAGAAAGGGTATTAGGCTGCAGGGAG
GGCAGGGCTGGGACCGAAGGGACAGTCCCTTCATCCTTGGTGTGAGTTTCTG
AACCTTGGTGCACAGAGATAAAAGTGAAGAAGTGTGTTAGGTGAGATGACTAAATTATGCC
CAAGAAAAAAAAAAATTAAAGTGTCTTCTGGGTCAAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPIKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKEIDFLCGWSLSERFGLLGGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRNVSAYDCTLNFRNNENPTILLGVNLNGKK
YHADLYVRRIPLEDIPEDDECSAWLHKLYQEKDADFQEEYYRTGTFPETPMVPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYNSDS
KQKLND

FIGURE 94

CTGAGGGCCCGGTAGC**ATGG**AGGGGGAGAGTACGTGGCGGTGCTCTCGGGCTTGCTCG
 GCGCACTCGTTCCAGCACCTAACACGGACTCGGACACGGAAAGGTTCTTCTGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTA
 TACAATTGACATTAGAAAATATTCCATGCTATCAGCTTTAGCTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTACAAATGCTAAAAGAATGTGGTAGGT
 TGGTACAAAATTCCGCGTCATTCAAGATCAGATCATGACGTTAGAGAGAGGCTGCTCACAA
 AAACCTGCAGGAGCATTTCAAACCAAGACCTGTTTCTGCTATTAAACACCAAGTATAA
 TAACAGAAAAGCTGCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAGGACTT
 TTTCACAGGGTACCTTAGGGTCCAATCTGGCATGTCGAACAACGTGGTTATAAAC
 TGTTACGGTTCTGTATGTCCTAGGTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTGAGAAGAGATGGATCCTAAAGGAGGTACATAAGATAAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGGAGACAGTGAACAAGCAGTAGATAAAACT
 AGTAAAGGATGTAACAGATTAAAACGAGAAAATTGAGAAAAGGAGAGGAGCACAGATTCAAG
 CAGCAAGAGAGAAGAACATCCAAAAGACCTCAGGAGAACATTTCATGTCAGGCATTA
 CGGACCTTTTCCAAATTCTGAATTCTTCATTATGTGTTATGCTTTAAAAAATGACA
 TGTTCTAAAGTAGCTGTAACTAACACCACATCTGATGTAGTAGACAAATCTGACCTAA
 TGGTAGAACACACTGACATTCTGAAGCTAGTCAGCTAGTACACCACAAATCTAAC
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTGGTTGTTAGATAACAAAGA
 CAAACGATCTAAAGCAAAACTGGTAGTAGTAACCAAGATAAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAAATTGAAAAGATGAAGGGTTGGTGAATTACCGGCTCTACAA
 TTT**TGA**CTTTAACCTACAAGGAGATTTTATTGGCTGATGGGTAAGCCAAACAT
 TTCTATTGTTTACTATGTTGAGCTACTGCAGTAAGTCTATTGTTTACTATGTTCAAC
 CTGTTGCGATAATACACAGATAACTCTTAGTGCATTACTTCACAAAGTACTTTCAAAC
 ATCAGATGTTTATTCCAAACCTTTTACCTTCACTAACATTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTAAAGTGGAAAAGTGGAGACCAAGGACAGTGGCTCACACCTGTA
 TCCCAGCACTAGGGAAAGACAAGTCAGGAGGATTGAGCTAGGAGTTAGAGACCAAGCC
 TGGGCAACTATTGAGACCATGCTTAAAGAAAATGAAAAGTGTGAGTCATTAAATCTCCTTAAG
 TTCAAAATATGAAAAGAAAATTATGAAAATTATGAGTCATTAAATGCTGGATATCATGCA
 TGATACTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTGCAAAACATCATCTAAATTAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVGWYKFRRHSQIMTFRERLLHKNLQEHE
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVANLGMSEQLGYKTVGSC
MSTGFSRAVQTHSSKFFEEDGSLKEVHKINEMYASLQEELKSICKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAREKNIQKDPQENIFLCQALRTFPNSEFLHSCVMSLKNRHVSCKSS
CNYNHHLVDVDNLTLMVEHTDIPPEASPASTPQIIKHKALDLDDRWFKRSRLLDTQDKRSKA
NTGSSNQDKASKMSPETDEEIEKMKGFGHEYSRSPTF

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FIGURE 96

GGCACAGCGCGCGGGAGGGCAGAGTCAGCCGAGCGGAGTCCAGCGGACGAGCGGACCAGGCAGGGCAGC
 CCAAGCAGCGCGCAGCGAACGCCCGCCGCCACACCCCTTGCGGTCCCCGGGCGCTGCCACACCTTCCTC
 CCTTCCCCGGCTCCCCGGCTCCGCCGGGAGTCAGCTTGCGGGGTTGCGTCCCCGGGAAACCCCGAGGTGACCA
 GCGCCGCGCTCTGCTTCCCTGGGGCGGGCCCTCAAGGCCCTCTTCTCCCTGGCCGGGCCCTGGCACC
 GGGGACCGTTGCGCTGAGCGGAGGGCCCAGCTACTCTAGTCCCCGACTCCGCCAGCCCTGGCCCTGGCGTAG
 CAACTCCAATCCTCTCCCTCCAGCTCACTCGTAGTCCCCGACTCCGCCAGCCCTGGCCCTGGCGTAG
 CGCGCGTCCCGTCCGGTCCAAAAGGTGGAAACGGCTCCGGCCGGCCGGCACCA**TGG**CACTGGCTTGGC
 CGCGCTTCTGCAACCTCGGAGTGTCTCAGCGCCGGCTGCTGCTGCCAGGCTCAAGTCGAAAAGTTGCTCGG
 AAGTGGCACCGTCTTACCTGTCAAAGGCTTCAACAGAACGATGCCCTTCCAGAGATCAAGGTGATCAT
 TTGAAGATCTGCTGAGGTTCTACCTGCTCTCAAAGGATGAGGAGAAGATACAGCGCTGCAAAGTAAGA
 TGATAATCTCAAAGAACTACTTGAAAATCGAGAGAAATCCCTGAATGATGATGTTGAGGACATATGGCCAT
 TTAATACATGCAAAGAAATTCTGAGCTTAAAGATCTTCTCGTAGAGTTGAAAGCTACTACGTTGGGAAATGT
 GAACACTGGAAAGAAATCTGAAATGACTCTGGCTGCGCTCTGGAGGGATGTTCCGCTGGTGAACTCCCAT
 ACCACTTACAGAGTATCTGAGTGTGAGCAAGTATCGGGAGCAGTGAGGCCCTTGAGGATGTCCT
 CGCAAATTGAAGCTCCAGGTTACTCGTCTTGTAGCACGGCTACTTTCGCTCAAGGCTTACGGGTTGGGG
 AGATGTCGTGAGCAAGGTCTCCGTGTAACCCCAAGCGCCAGTGTACCCATGCCCCCTGGAGATCTACT
 GCTCCCACTGGGGCTCTGAGCTGTGAGGCCATGTTACAACACTGCTCAAACATCATGAGGGCTGTTG
 GCCAAACCAAGGGATCTGAGATGAAACAAATTCTAGATGCTATGCTGATGGTGGCAGAGGGCTAGA
 GGGTCTGACCAAATCTGAGTGTGAGCTGATGCTGATGAAAGATTCTGATGCTATGAACTGAGCAG
 ATAATAGTGTCTCAAGGTTTCAAGGAGTTTCAAGGGATGTGGGACCCCCAAAGCCCTCCAGCTGGACGAAATT
 TCTCGTCCATCTGAAAGTGCCTCAGTGCCTCGGACACCATCACCCGGAGGAACGCCAACACAGC
 AGCTGGCACTAGTTGGACCCGACTGGTTACTGATGTCAGGAGAAACTGAAACAGGCCAAGAAATTCTGGTCT
 CCCCTGGACCAACCTTTCAGATGAGGGATGGTGCAGGAAACGGCATGAGGATGACTGTTGGAAATGG
 AAAGGCAAAAGCAGGTACCTTTCACTGAGCAAGGAAATGAAATTAGGCAACAGGGCAACACCCAGGGTCA
 GTTGGACACAGCAACAGCATATGATCTTCTGTCAAATCATGCTCTGGAGTGTACACAGCAAGATGA
 AGAATGCAATCAGATGGGACAGCTGGACTCTTGTGATATCAGTGTGAAAGTAGTGGGAGAAGGAAGTGG
 GGCTGTGAGTACAGCAGTGGCTTCAAGAGTTTACTACATGGCAGTGCACATGCTGGAGAGTGGCAATGA
 GAAAGCCGACAGTGTGGTCTGGGACAGGCCACTCCACTGCTTGTTCTGATCAGTGGGAGAGTGGCACTTGG
 TTATGCAAGAGAGTGGGAGA**TAAT**CTCAAACCTCTGAGAAAAGTGTCTCAAAAGGTTAAAGGCACAGGT
 ATCACTTTTCTACCATCTTGTACTTCTCTTTAAATGATGACAACTGATGCTTCTACTATGTC
 CACTGGTTTAAGAAGTGTGACTTTGTTCTCATTGAGTTGGGAGGAAAGGGACTGTGCAATTGAGTTGG
 TCCCTGCTCCCCAAACCATGTTAAACCTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTCATTGG
 TTTTATCACTTATTATTGTTGTTGATGTTTTCTCATTTCGTTGTTGTTTTCTCAACTGTGATCT
 CGCCTTGTTCTAACAGCAAACCGGGTCCCTCTGGCACGTAACATGTACGTTATCTGAAATATTAAATA
 GCTGTACAGAACGAGGTTTATTATCATGTTATCTTATTAAAGAAAAGGCCAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAEELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLTERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFGDPRKLKLQVTRAFVAARTFAQGLAVAGDVSKVSVNPTAQCTHAL
LKMIYCSCRGLVTVKPCNYCSNIMRGCLANQGDLFEWNNFDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFGCGPPKELPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSLPSNCNDERMAAGNGNEDDCWNGKGKSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVFFFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

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FIGURE 99

MKVLISSLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

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FIGURE 100

AATGGCTGTCTTAGTACTCGCCTGACAGTTGTCTGGGACTGCTTGCTTATTCCTGACCT
GCTATGCAGACGACAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGAAAGACCA
AAGCCAGACTTCCCCAATTCTTAAGCCTCTGGGACAGAGATCATTGAGAATGCAGTCGA
GTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTATGGAATTGATGATAATGAAGGAA
AACATTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCTGGACAATCCAAGAGCA
GCCAAATCTGCTTTCCAGTTGGCTCCACAAGTCCTCCAGGACAGAGGCCCTAAAGCAAC
TCCCACGAGTTCTCAGGATTCAAGGCTCTGGCTCAACCAAACAGAACTCATTTGAACACC
CTGACTGCATTTTGCTTTAGAAAGTTAGAATAAATATGGCGCTTGGGATCACATAGTTG
ATGGAGAGGAAA

FIGURE 101

MAVLVLRLTVVVLGLLVLFLTCYADDKPDKPDDKPDSSGKDPKPDFPKFLSLLGTEIIENAVE
FILRSMRSRSTGFMEFDDNEGKHSSK

FIGURE 102

GGAGGCCAGCGCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGC~~CCCAGCGGAAGCACAGCT~~
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACCTCTGCAGCTGCTGGTGTGCTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGCTGCTGGCAGCCCCGTGCAAAGCTACTTCC
 CCTACCTGATGGCGTGCTGACTCCAAAGAGCAACCGAAGATGGAGAGCAAGAACGGGAG
 CTCTTCAGCCAGATAAAGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACTTCAAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCACCTTGAGAAGTCCTGACAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTGTGGTGGCTCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCATGGATGT
 GGTGGTCTGCACTCTGGTGTGCTGTGCAAGGCCAAGGAAGGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTCTGGGAGCATGGCAGAACATATGGA
 AGCTGGCCTTCATGTGGCAGCAAGTTTCGAGGCCACCTGAAACACATTGGGATGGCTG
 CTGCCTCACAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAATGG
 AACGACAGCCCCCTCCCTGAAAGTGGCTACCTGTTGGGCCCCACATCATGGAAAGGCTGTC
 AAACAATCTTCCCAAGCTCCAAGGCACTCATTGCTCCTTCCCAAGCCTCCAATTAGAAC
 AGCCACCCACCAGCCTATCTATCTTCACTGAGAGGGACCTAGCAGAACATGAGAGAACATT
 CATGTACCCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGCAATCTTAACCTCAATC
 CCGCCTCGACAGTGGAAAAGCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTTGTATCCTCAACTGCAAGTTCTGGACTAGTCTCCCAACGTTGCCTCCCAATGTTGTC
 CCTTCCCTGTTCCCATGGTAAAGCTCTCTCGCTTCTGAGGGCTACACCCATGCGT
 CTCTAGGAACCTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
 CTCCCCACTACCACCTCTTCCCTGAGCTGGGGCACCGGGAGAACATCAGAGATGCTGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTGTTCTCAAATATTTTAATAATAGACGA
 AACCAACG

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FIGURE 103

MDILVPLLQLLVLLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMVVVCTLVLCVQSPrKVLIQEVRVLRPGGVLFWEHVAEPYGSWAFM
WQQVFEPTWKHIGDGCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYLPLRGT

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FIGURE 104

GTGGGATTTATTGAGTGCAAGATCGTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG
 CAGATGTTGGGCTTGTCCGAACAGCTCCCTGCCCAGCTCTGTAGATAAGGGTAAAAA
 ACTAATATTATATGACAGAAGAAAAG**TGA**TGTCATTCCGTAAGTAAACATCATCTTGG
 TCCTGGCTGTTGCTCTTCTACTGGTTTGACCCATAACTCCTCAGCTTGAGCAGTTG
 TTAAGGAATGAGGTTACAGATTGAGGAATTGAGGCCCTAACCTATAGACTTGTCCAAA
 TGCTCTCGACATGCGAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGATCTG
 AAGACAGGGCTTGGGGGGCATTCGAGCTATAAACAGCATTGAGCACAAACACTCGCTCCAAT
 GTGATTTCTACATTGTTACTCTCAACAATACAGCAGACCCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATAAAAATTGTCATTTGACCCCTAAACTTGGAAAGGAA
 AAGTAAGGAGGAGATCTGACCAGGGGAATCCATGAAACCTTAAACCTTGCAAGGTTCTAC
 TTGCCAATTCTGGTCCCAGCGAAAGAAGGCCATATACTGGATGATGATGTAATTGTGCA
 AGGTGATATTCTGCCCTTACAATACACACTGAAGCCAGGACATGCACTGCATTTCAAG
 AAGATTGTGATTCACTGCTCTACTAAAGTTGTCATCGTGGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAGGAAAGAATTGCAAGCTTCCATGAAAGCAGCAGCTTG
 CTCATTTAATCTGGAGTTTGTGCAAAACCTGACGGAATGAAACGACAGAATATAACTA
 ACCAACTGGAAAATGGATGAAACTCAATGTAAGAAGGGACTGTATAGCAGAACCTGGCT
 GGTAGCATCACAACACCTCCTGCTTATCGTATTGATTTATCAACGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTGGTCCAGTGCTGGAAAACGATATTCACCTCAGTTGTAA
 AGGCTGCCAAGTTACTCATTGGATGGACATTGAGGCCATGGGAAGGACTGCTTCATAT
 ACTGATTTGGGAAAATGGTATATTCCAGACCAACAGGCAAATTCAACCTAATCCGAAAG
 ATATACCGAGATCTCAAACATAAAG**TGA**AACAGAATTGAACTGTAAGCAAGCATTCTCAG
 GAAGTCCTGGAAGATGAGCTGGAAAGTAACAGTGCTAGGCTCAATGCCCTATCGGTA
 GCAAGCCATGGAAAAGATGTGTCAGCTAGGTAAGATGACAAACTGCCCTGTCAGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCCTCATGCCCTACCAAGTGTGTTCTT
 ACTACAATGCTGAATGACTGGAAAAGAAGAACTGATATGGCTAGGTCAGCTAGCTGGTACAGA
 TAATTCAAAACTGCTGTTGGTTAATTGTAACCTGTCAGCTGATCTGAAATAAAACTT
 ACATTTTC

FIGURE 105

MSFRKVNIITLVLALVALFLLVLHHNFLSLSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIASEDRLGAIAAINSIQHNTRSNIFYIVTLLNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDASTKVVIRGAGNQNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRNQITNQLEKWMKLNVEEGLYSRTLAGSITTPPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKAALKLHWNGHLKPWGRTASYTDWWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTGCCCATAAATCCCTCAGCTTGAGCAGTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCTCAACCTNTAGANTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTGGGGGGCCAT
TGCAGCTATAAACAGCATTAGCACAAACACTCGNTCCAATGTGATTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGCTCTGGNTAACAGTGAATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTGACCTAAACTTTGGAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTAACCTTGCAAGGTTCTACTTGCCAATTCTGGTTCCAGCG
CAAAGAAGGCCATATACATGGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTCAGAAGATTGTGATTGCAGCCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTCAGGGAACGCAGGGCGGCCAGACAAACGGGC
 TGGGCTCCGGGCTCGGGCGGGCGTGAGCTGGCAGGGCGGGTGGGGCGCGGGCTGCA
 TCCGCATCTCCATCGCCTGCAGTAAGGGCGGCCGCGCGAGGCTTGAGGGAACGACT
 TGTCGAGGCCAACAGGGGTGTCCTGAGCTGGTGGGATCCCCGGAGCGTCACATCACT
 TTCCGATCACCTCAAAGTGGTAAAAACTAATAATTATATGACAGAAGAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTGGCTCTGGCTGGTGTCTCTTACTGGTTTGAC
 CATAACTCCTCAGCTGAGGAGTTAAGGAATGAGGTACAGATTCAAGGAATTGAG
 GGCCTCAACCTAAGGACTTGTCCAAATGCTCCGACATGCAGTAGATGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTGGGGGCCATTGCA
 ACAGCATTCAAGCACAACTCGCTCAAATGTGATTCTACATTGTTACTCTCAACAATACA
 GCAGACCATTCCGGTCTGGCTCAACAGTGATTCCCTGAAAGCATCAGATA
 AAAATTG
 TCAATTGGACCCCTAAACTTTGAGGAAAGTAAAGGAGGATCCTGACCAGGGGAATCC
 ATGAAACCTTAACTTGCAGGTTCTACTTGCAATTCTGGTCCAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTCAAGGTGATATTGCCCCTTACAATACAGCA
 CTGAAGCCAGGACATCGAGCTGATTTCAGAAGATTGATTCAGCCTACTAAAGTGT
 CATCCGTGGAGCAGGAAACCGTACAATTACATTGGCTATCTTGACTATAAAAGGAAAGGAA
 TTCGTAAGCTTCCATGAAAGCCAGCACTTGCTATTAACTCTGGAGTTTGTGCAAAC
 CTGACGGAATGGAAACGACAGAAATATAACTAACCAACTGGAAAAATGGATGAA
 ACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCTGGCTGGTAGCATCACACACCTCTGCTTATCG
 TATTTTATCACAGCACTCTACCATCGATCCTATGTGGATGTCGCCACCTGGTCCAGT
 GCTGGAAAACGATATTCACCTCAGTTGTAAGGCTGCAAGTTACTCCATTGGAATGGAC
 TTTGAAGCCATGGGAGGACTGCTCATATACTGATGTTGGGAAAAATGGTATATTCCA
 GACCCAAACAGGCAAATTCAACCTAACCAAGGATACCGAGATCTCAAACACATAAAGT
 GAAA
 CAGAATTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAGATAGCATGCGTGGGAG
 TAACAGTTGCTAGGCTCAATGCCATCGGTAGCAAGGCCATGGAAAAGATGTTGTCAGCTAG
 GTAAAGATGACAAACTGCCGTGGCAGTCAGCTCCAGACAGACTATAAGACTATAAA
 ATGTCCTCATCTGCCATTACCAAGTGTGTTTACTACAAATGCTGAATGACTGGAAAGAAGA
 CTGATATGGCTAGTTCAGCTAGTGGTACAGATAATTCAAAACTGCTGTTGGTTTA
 GTAACCTGTGGCCTGATGTAAATAAAACTACATTTCATAGGTA
 AAAAAA

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FIGURE 108

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
 GAAGGCCGGCATACCAGACTCCTGCCATGGGCCTCACCATGGAGGCAGCTCCACTG
 TCTGTGCTGGTCTGAGGGTGTGCCGTCAATGGGGCAGCCATCTCCAGGGGCCCTCATC
 GCCATCGTCTGCAACGGTCTCGTGGCTTCTGCTGCTGCTGGTCATCTCTGCTG
 GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTGAATCCAGTCCAACCTCAGCCC
 TGGCCCTGTCTGAGAAGGCCCAACCCCCAGAACGCCAGCCATGAAGGCAGCTACCTGC
 TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCAGGACTAAGTCCACCTCACCTAGAG
 CCTGGAATTAGGATCCAGAGTTCAGCCAGCCTGGGTCCAGAACTCAAGAGTCCGCTGCT
 TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTGGCTCCAAATAGGAGCTCAGTGGCCC
 TAAGGAGATGGGCTGGGTGGGGCTTATGAGTTGGTGTAGAGCCAGGGCCATCTGGACT
 ATGCTCCATCCAAAGGGCCAAGGGTCAAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC
 TCTAGGCCCTCTAGGTTGGGAAGCAAACGGAACCCATGGCAATAATAGGAGGGTGTCCAG
 GCTGGGCCCTCCCTGGTCTCCAGTGTGGATAATAATGGAACTATGGCTCTAA
 AAAAAAAAAAAAAAAA

FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSNPVPTPALAPVLRRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

FIGURE 110

GTTTGAATTCCCTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTCCTTATTAACCGATGTGTCCCCTCAAAACACCTGAGTGCTA
 CTCCCCTATTCGATCTGTTGATAATGATGTTGACACCCTCACCGAATTCTAAGTGGAA
TCATGTCGGGAAGAGATACACATCCTGGCCTGTATCCTCGCATTAGCCTGTTGGCC
 ATGATGTTACCTCAGATTCATCACCAACCCCTCTGGTCACATTTCATTTCATGGTTAT
 TTTGGGATTGTTGTTGTCGCGGTGTTTATGGGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAACATGGACACAGAAAGGGAAATATGAAGTGCCTGGGGTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTCGTCTGATTTGTTCTCAGAAAGAGAAATAAAATT
 GACAGTTGAGCTTCCAAATCACAAATAAGGCCATCAGCAGTGCTCCCTCTGCTGTTCC
 AGCCACTGTGGACATTGCCATCCTCATTTCTCTGGGCTCTGGGTGGCTGCTGCTG
 AGCCTGGGAACTGCAGGAGCTGCCAGGTTATGAAAGGGCCAAGTGGAAATAAGCCCC
 TTCGGGATTCGGTACATGTGGTGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCAGCAAATGACTATAGCTGGGCAGTGGTTACTGTTATTCAACAGAAAGT
 AAAAATGATCCTCCTGATCATCCCATCCTTCGTCCTCTCCATTCTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCAATTAACTCTGTGGTAGGAGTCAGAACATCATTGTC
 TGTCATGCAAAACGCACTGAAAGAACAGCAGCATGGTCATTGTCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTCTGGTGTCTGACAATACCTGCTCCATCTCAACCGAAATGCATA
 TACTACAACGTATTAAATGGGACAGATTCTGTACATCAGCAAAGATGCAATTCAAATCT
 TGTCAGAAACTCAAGTCACATTACATCTTAACTGCTTGAGACTTCATAATTTC
 GGAAAGGTAGTGGTGTCTGTTACTGTTGGAGACTCATGGCTTTAACTACATACATCG
 GGCATTCAGGTGTGGCAGTCCCTGTTATTGGTAGCTTTGGCTACTTAGTGCC
 ATAGTTTTATCTGTGTTGAAACTGTGCTGGATGCACTTTCTGTGTTTGCTGTTGAT
 CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTATGGATCAAGAATTCTGAGTT
 CGTAAAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCAGTCAATTAAAGGA
 ATGAGGAGGAAACAGAACTCCAGGCCATTGTGAGA**TAGAT**ACCCATTAGGTATCTGTACCT
 GGAAAACATTCCCTCAAGAGCCATTACAGAAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTAAAGACCTAATAAACCTATTCTCCTCAAAA

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FIGURE 111

MSGRTILGLCILALALS LAMMFTFRFITTLLVHIFISLVLG LLVM FVCGV LWL YYD YTN DL
SIEL DTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFL FQ
PLWTFAILI FFWVLWAVLLSLGTAGAAQVM EGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCYC CFWCLDKYLHLNQNAYTTAINGTDFCTS AKA DF KIL
SKNSSHFTSINC GDFIIIFLGKV L VVCFTVFGGLMAFNYNRAFQVWAVPLLVAFFAYLV AH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFV KR SNKL NNARAQQDKHSLRN
EEGTELQAIVR

FIGURE 112

GTTCGATTAGCTCTCTGAGAAGAAGAGAAAAGGTCTTGGACCTCTCCCTGTTCTCCTT
 AGAATAATTGTATGGATTGTGATGCCAGGAAGGCTAAGGGAAAAAGAATATTCAATTCTG
 TGTGGTGA AAAAATTTTGAA AAAAATGGCTTCTCAACAAAGGGTGTCAATTCTGATATT
TATGAGACTGTGTTCACTATGAAGGCATCTGTATTGAATGTTCTGTTGCTGG
 TGACTGGAGTACATTCAAACAAAAGAACCGGAAAGAGATTAAAGGGCCCAAGGTTACTGTG
 CCTCAGATCAACTCGATGTAAGCGGGAAAGATCATCGATCTGAGTCATGTGAAATG
 TCCAGCAGGATGCCAAGACCCCCTAACACATTGTTATGGCAGCTGACGTGTATGCATCTTACT
 CCAGTGTGTTGCGCTGCCCTACACACTGGTGTCTGATAATTCAAGAGGGAAAATACTT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAGGGAGTTATTCCAACCGTGCCAAATCGTT
 ATCCCTAACACAGGATGGAGAAATCTTATCGTCTTAGAGAATGAAACCCAAAAGGCTGAA
 CCTACCCATCAGCTTCACTACATCATCGAAAAGTCCAGTGCCCAAGCAGGTGAGACC
 ACAAAAGCCTATCAGAGGCCAACCTATCCAGGGGAAACTGACGGCCAGCAGCGTACTCTGCA
 GCTTCGCGTGTACTGTAGCTGGCACCCCCAACCTTGCAAGGCCATCCTCTG
 CTGCTTCTACACCACGATGCCAACGACCAAACTAGTGGGCCAACAGGAGGAGATGGAT
 CTCGGTCTACGACGCCAACAGCAGGAGCTGATCCAGGAAACAGGGCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCTTCAGGGAGCTGCCCTCAGAAACCTGTTGGAGCGGGATGTCAGCTGGGAC
 TTGTTCCAAAAGAAGAATTGAGCACACAGCTTGGAGCAGTATCCCTGAGATCTCG
 TGCAAAATTGACTGTCGTTTAAATTGATGGAGCACCGCATGGCAACAGGGCATTCCG
 AATCCAGAAGCAGCTCTGGCTGTGTTGCCAACCTGCACTTAACTCAAGGACACACAG
 TGATGGGTGTGTCAGATGGAGACAACCTGCTACTCACTTAACTCAAGGACACACAG
 AATTCTCGAGATCTGAGAGAACGCCATAGAGAAAATTACTCAGAGGAGGACTTCAATGT
 AGGTCGGGCCATCTCTTGTGACCAAGAACATTCTTCAAAACCCATGGAAACAGAGCG
 GGGCTCCAAATGTGGTGTGGTGTGGATGGTGGATGGCTGGCCACGGACAAAGTGAGGAGGCT
 TCAAGACTGTCGAGAGACTCAGGAATCAACATTCTTCATCACCATGGAGGTCTGCTGA
 AAATGAGAAGCAGTATGTGGTGAGGCAACTTGGCAAAACAGGCCTGTCAGAACAAACG
 GCTTCATCTGCTCCACGTCAGCAGACTGGTGGCCCTGAGAACGACCTCTTGAACCTGGCTG
 AAGCGGGCTGCGACACTGACCCTGGCTTGAGCAAGAACGACTCTTGAACCTGGCTGACAT
 TGGCTCTGTCATCGAGGCTCAGCAGTGTGGAGCAGGCAACTTCCGACACGGCTCTCAGT
 TTGAGCAGGACATCCAGGACATTTCAGACTTGGAGATGGCAGACAGCAGCAGTC
 CAGTACACCTACGAAACAGCGGCTGGAGTTGGTGTGACAAGTACAGCAGCAAGCTGACAT
 CCTCAACGCCATCAAGAGGGTGGCTACTGGAGTGGTGAGCACCGCACGGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTTCAAGAACGTCAGGCAACAAAGAGGAATTATGATCCTC
 ATCACCGAGGGAGGCTCACGACGAGCTGGGATCCCAGCCATGGCTGCCCATCTGAAGGG
 ATGATCACCTATGGCATAGGCGTTGGCTGGGCTGAGAACGACTTGGAGGAGCTAGAA
 GATCTGGCAACCTCCATCAGTGTGACAGGAGCTTGGAGGAGCTTGGAGGAGCTTGG
 CTCACCCGGCAGAGAACCACTCTTGTGGAGCAGATTGACAACCTCCATCAGTATGTC
 CCCAGGATCATCAGAACATTCTACAGACTCACAGCTGGAACT**TGA**ATTCAAGAG
 CAGGCAGAGCACCAAGCTGCTTACTAAGTACGCTGGGACCCACCGCTTAA
 TGGGGCACGCCACGGTGCATCAAGTCTGGCAGGGCATGGAGAAAACAAATGTTGTTTATT
 TTCTTGGCCATCATGCTTTCAATTCAAACATTGGAGTTACAAAGATGATCACAAACGT
 ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTCTGGAGGAGATTTCACATTGACAATT
 GTTTCAAAATAAATGTCGGAATACAGTGTGAGCCTTACGACAGGCTTACGTAGAGCTTT
 GTGAGATTGTTAAGTGTATTCTGATTGAACTCTGTAACCCCTCAGCAAGTTCATT
 GTCATGACAATGTAGGAATTGCTGAATTAAATGTTAGAAGGGATGAAAAAATAAAAAAA
 AAAG

FIGURE 113

MRTVVILTMKASVIEMFLVLLVTGVHSNKETAKKIKRKPKFTVPOINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVGTDVYASYSSVCGAAVHSVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPSPSAASTTSIIPRPQSVGHRSQEMDLWSTATYTSSQRNPRADPGIQ
RQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLVKVCDTDRLLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKFEIISDTDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNIAIKRVGYWSGGTSTGAAINFALQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRITQNICTEFNSQPRN

FIGURE 114

CAGGATGAACTGGTGCAGTGGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTA
TGCCTTCCGGCTGCTCATCCCGCTCGGCCCTGTGCGCGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCACGGCTCCGCGCCAGATCCGCCACTACAGTTTCTGACTCTAA
 TGATGCACGGACACCTTGCTGATTTGGGAATGTCAGAATTCAAAGAGTGGTTGAAG
 TGCTCAGGACAGCTGGACTTGATATTGATGTGAACGCCCTGTGTTGAAACAACATT
 CGAGTGGTAGGAGGACTCCTGTCATCTGCTCCAAGAAGGCTGGGTGGAAGTAGA
 GGCTGGATGCCCTGTCCGGGCCTCCTGAGAATGGCTGAGGAGGCGGCCGAAACACTCC
 TCCCAGCCTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACTTACTTCATGGCGT
 AACCCAGGAGAGACCCCTGTCACCTGTACGGCAGGGATTGGGACCTTCATTGTAATTGC
 CACCCCTGAGCAGCCTCACTGGTGACCCGGTGTGCAAGAATGTGGCCAGAGTGGCTTGATGC
 GCCTCTGGAGAGCGGTCAGATATCGGGCTGGTGGCAACCACATTGATGTGCTACTGGC
 AAGTGGTGGCCAGGACGCAGGATCGGGGCTGGCGTGGACTCTACTTGGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCCGAACTACACCCGCTTCGATGACTGGTACCTGTGGGTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTCCAGTCCTGGAGGCCTACTGGCCTGGCTTCAGGCCATTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAACAGTGGGG
 GGCTCCCGAATTCTACAACATTCTCAGGGATAACAGTGGAGAACGGCAGAGGGCTACCCA
 CTTCGGGAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGGCACGGGGATCCACCCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAAATCAGCAAGGTGGAGTGGG
 TTGCAACAATCAAAGACTGCGAGACCACAAGCTGGACAACCGCATGGAGTCCTTCTG
 GCCGAGACTGTGAAATACCTCTACCCCTGTGGACCCAACCAACTCATCCACAACATGG
 GTCCACCTTCGACGGGTGATCACCCCTATGGGAGTGCATCTGGGGGCTGGGGGTACA
 TCTTCACACAGAAGCTCACCCATCGACCTTGCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGGTGGAGGACTGTGAGGGAAATTCTACTCTCAAAACGGAGCAGGTC
 GAAATTCTGAAAAAAACACTGTTAGTCGGGCCATGGGAACTCCAGCAAGGGCAGGAACAC
 TCTTCTCACCGAGAAAACCATGACCAAGGGAGAGGAAGGCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCACTCAGGCCCTCACCTCAAGTGGCATTACTGGGACAGGTTTCT
 AGACTCCTCATAAACACTGGATAATTTTTATTTTTATTGGGAGGCTAAACTATAATA
 AATTGCTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAFDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASFETNIRVVGILLSAHLLSKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQPTGMPYGTVNILLHGVPGETPVTCAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLAMFLEYNK
AIRNYTRFDDWYLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIIPQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQLKEEQWEVEDLMREFYSLKRSRSKFKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTCTCTGGAACTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTG
 GGCAGAAAGGAGGGTCTCGGAGCCGCCCTTCGAGCTCTGGCCGGCTCTAGAACAA
 ATTCAAGGCTTCGCTCGACTCAGACCTCAGCTCAAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTATTTGAAAGAACAAATGTTCTAGGTCAAACGTGAGTCTACCA
AATGCAGACTTTACAATGGTCTAGAAGAACATCTGGACAAGTCTTTCATGTGGTTTCT
 ACGCATTGATTCCATGTTGCTCACAGATGAAGTGCCCATTGCCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTTGTATGTTGAGGCCAGTGATCGCCCTGGAGA
 AACAGTGTACTATTCTGTCGAATACCAGGGGAGTAGCAGAGAGCCTGTACAGAGCCACATCT
 GGATCCCCAGCAGCTGGTCTCACTCACTGAAGGCTCTGAGTGTGATGTCAGTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCTGTCAAGGGCACATTGGCTCACAGACCTCAGCCTG
 GAGCATTCTGAAGCATCCCTTAATAGAAAACTAACCACATCCTACCCGACCTGGGATGGAGA
 TCACCAAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGCCCCAGTTGAGTTG
 CTTGTGCCACTGGAGGAGGGAGCTGGTCCGGAGAACATGTCAAAATGGTGGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGCTGCACTGTGTAAGGCCAGA
 CATTCTGAAGGCCATTGGGAGGTACAGGCCCTCAGCCAGACAGAACATGTGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTGCCCTTGTGGCTCATGCTGATCCTGT
 GGTCGTCGCACTGTCGCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGGCCCTGG
 TGTCCTCCAGACACCTTGAAAATAACCAATTCAACCCAGAAGTTAACAGCTGCAAGAAGG
 GAGGAGGGTGGATGCCTGTGCCACGGCTGTGATGTCCTGAGGAACCTCAGGGCTGGAT
 CTCA**TAG**TTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAAC
 ATGAGGGACAAGTTGTTCTGTTCCGCCACGGACAAGGGATGAGAGAACATGAGAAGA
 GCCTGTTGCTACAAGTCTAGAAGCAACCATCAGAGGAGGGTGGTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTGCTGGTGAACCA
 CTGGGAAAAGTGAACCTCATCCCTCGGTCTAACAGTTCTCATGTAATGGGAAATTACC
 TACACACCTGCTAAACACACACACAGACTCTCTCTATATATACACACGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGCACACTCAGTCTGACTGATTGAG
 TGTTCCTGGAGAGCAGGACATAAATGTATGAGAACATGATCAAGGACTCTACACACTGGG
 GGCTTGGAGAGGCCACTTCCCAGAATAATCCTGGAGAGAACAGGAATCATGGGAGCAATGG
 TGTTGAGTTCACTCAAGCCCAATGCCGGTGCAGAGGGAAATGGCTTAGCGAGCTACAGT
 AGGTGACCTGGAGGAAGGTCAAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACTACTGTAAGTGTGACAGTGTGTCACACTGCAGACAGCAGGTGAATGTATGT
 GTGCAATGCGACGAGAACATGCAAGACTGAGTCAACATGTGCATGTTGTTGCTCCTTTTC
 TGTTGGTAAAGTACAGAAATTCAAGCAATAAAAGGGCCACCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFMVLEEWTSFLMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGE
TVYYSVQEYESLYTSHIWIPSSWCSLTEGPECVDTDDITATVPYNLVRATLGSQTSAW
SILKHPFNRSNSTITRPGMEITKDGFLVIELEDLGQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAFVGFMLILV
VVPLFWKMGRLLQYS CCPVVVLPDTLKTNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGTTGGCAAAAGGAGGTTGCTCGAGCCGCCCTTCTAGCTT
CCTGGCCGGCTCTAGAACATTAGCAGCTCGCTGGACTAGACCTCAGCTCAAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTATTTGGAAAGAAACAATGTTCTAGG
TCAAACGTGACTACCAAATGAGACTTCACAATGGTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTCTACGCATTGATTCCATGTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACCTCTGTACTCTAACCAACATGAAGCATCTTGATGTGGAGGCCA
GTGATCGCGCCTGGAGAACAGTGTACTATTCTGTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATGGATCCCCAGCAGCTGGTGTCACTCACTGAAGGTCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTGTGTCAAGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCTGAAGCATCCCTTAATAGAAACTAACCATCCTTAC
CCGACCTGGATGGAGATCACAAAGATGGCTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTGAGTTCCTTGTGGCTANTGGAGGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCAGCCGCTGGGTATCTCGAGAAAAGAGAGGCCAATATGACCCAC
ATACTCAATATGGACCAANTGCTATTGTCACCTGTTGAGTGGCGCTGGGTTGAT

2011-11-11 12526660

FIGURE 119

CGGACGGTGGGCCACCTCGGAACAAGCC**ATG**TGGCGGCACGGTGGCAGCGCGTG
GCTGCTCTGTGGCTGGGCCCTGCGCCAGCAGGAGCAGGACTTCTACGACTTCAGGG
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGATCGGTGTCCTGGTGGT
AATGTGGCAGCGAGTGGCTTCACAGACCAGCACTACCGAGCCCTGAGCAGCTCAGCG
AGACCTGGGCCCCCACCACTTAACGTGTCGCCCTCCCTGCAACCAGTTGGCCAACAGG
AGCCTGACAGAACAGGAGATTGAGAGCTTGGCCCGCACCTACAGTGTCTCATTCCCC
ATGTTAGCAAGATTGAGCTACCGGTACTGGTGCCATCTGCCTCAAGTACCTGGCCA
GACTCTGGAGGAGGCCACCTGAACTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
TGGTAGGGCTGGGACCCAAGTGTCAAGTGGAGGAGTCAGACCCCAGATCACAGCCTC
GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTTA**TAA**ACCCAGCGTCTCCCTCCACCA
CCTCATCCGCCACCTGTGTGGGCTGACCAATGCAAACCTCAAATGGTCTCAAAGGGAG
AGACCCACTGACTCTCTTACTCTTATGCCATGGTCCCATCTCTTGTTGGGGAA
AAATTCTAGTATTTGATTTGAATCTACAGCAACAAATAGGAACCTCTGGCCAATGAG
AGCTCTGACCACTGAATCACCAGCGATCGAACAGTCTGCAACAAAATGTGTGGCAA
TAGAAGTATATCAAGCAATACTCCCACCCAGGCTCTGTAACCTGGGACCAATGATTAC
CTCATAGGGCTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCAGC
CAAATAGGAGGCAATTCAATGAACATTGGCATATAACCAAAAAAAACTGGTATCAAT
AAAAACTTGCATCCAACATGAATTCCAGCGATGATAATCCAGGCAAAGGTTAGTGT
GTTATTTCTCTGTATTATTTCTTCATTACAAAAGAAATGCAAGTCATTGTAACATCCA
AACAAATACCTCACGATATAAAATAAAAATGAAAGTATCCTCTCCTCAAAAA

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FIGURE 120

MVAATVAAAWLLLWAACAAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVVNVASECGFTDQ
HYRALQQQLQRDLGPHHFNVLAFCNCQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 121

CCGACGGCTGGGGGGGGGACGCAGGCCAAGCGAGCC**ATG**CTGTACGTGGGATGC
 TCGCCTGGGGAGGCTGCGCCGGAGCTGGGGTGTCCCCCTCCAGTTCCAGAGAGGTGGATCG
 CGGAGTTGCAGGAAGCCAGGTTGCAGGGTGTCCCCCTCCAGTTCCAGAGAGGTGGATCG
 CATGGTCCTCACGGCCATCGGAGGGCTCAGCTACGGTTCAAGGGGTGCACCAAAAGCATCTTA
 ACAGCAAGACTGTGGCCAGTCCTGGAGACACAGCACAGAGGGTCCAGAACGAGAGGCC
 TTGGTCCTCCATGAAGACGTCAAGTTGACCTTGCCCAAATCAAGGAGGAGGTGGACAA
 AGCTGCTCTGGCTCTGAGCATTGGCTATGCCAGTGGCAAGGTCAGGGCTGGGAC
 CTAACCTCATGAGCTGGTGTCTATGCCAGTGGAGTATGTCTCAAGAAGGGCTGCAA
 TCTGTGAACCCAGCTTACAGCTATGCCAGTGGAGTATGTCTCAAGAAGGGCTGCAA
 GGCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAAACTACAACGTCAGGAGCATCT
 GTCAAGGAAGTGGAGAATGCCAGCAGGGCTTGAAGAGTCAAGGGCTCCAGATGTGACC
 ACAGTCATCTGGTGTGATGCCCTTGCGGGGACCCCTGCTCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATGGACAGCTCAAATACAACCGCAGTTCTGTCTGCCATG
 ACCCCCATAACATCCAGTCACTCCGGGACAAACAGGCCAGCCCCAAGGGGGCACCTCTCC
 CACTACACATGTCAACAACTCCAACATTAGGAGAGCCTGAAACTGCTGAGAAC
 ACCAGAGCAGTGGGGATGATCTGCCAACCCCTGTACCATTCGCTGGTCCGGCAG
 GCACAATGATGTGTCATGTAACGGTGCACCCATCTGGCTCTCCATCTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGACCTTCTCTGTATGGTACCCCCAGAT
 GTTCGTTGGACATTCTGAGACCCAGCAACTTCTCAGATTGACATCTCGACCATGTTGGAG
 GTGTCATTCTGGGCCCCCTGACCTCCAGAGTTGATCCGAGGCCATCATCAACAGATAAAT
 ATGAAGGACCTGGTGTGTTGCTTATGGAACACAGAACAGTCCGTGACATTGCGCAGCT
 CCCTGAGGACACTGGAGCAGAACAGGAGAACAGCTGGCAGAATATGCTCACACGGAGG
 CCCGGATCATGAACATGGAGGAGCAGGGACGGCTGGCAAAGCTGAACACGCCGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGCTACTGGGTGAGCCTCAGAACAGAGGAGCAGT
 GGATCAGGACAAGTGTATTGGACAGGAGATGTCGCCAACATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGGCGCTAAGGATATGATCATCGGGGTTGTGAGAACATCTACCCCGAGAG
 CTCGAGGACTCTTACACACACCCGAAGGTGCAAGGAAGTGCAGGTGGGAGGTGAAGGA
 CGATCGGATGGGGAAAGAGATTTCGCTCATTGCGCTGAAGGACGGGGAGGAGACCCAGG
 TGGAGGAGATAAAAGCTTCTGCAAAGGGAGATCTCACTTCAGAACAGATCCAAAATTCGAGA
 GCAGATGGAACGACATCTAAATCT**TGA**ATAAAGCAGCAGGGCTGTCTGGGGTTGGCTT
 GACTCTCTCTGTCAAGATGCAACCTGGCTTATGACCTAGATGTCCCCAGCACCCAGTT
 TGAGCCAGGCACATCAATGTCAGGAATTGACTGAACGAACTAACAGAGCTCTGGATGGTC
 CGGGAACTCGCCTGGGACAAGGTGCAAAGGCAAGGAGCAGCCTGCCAGGCCCTCCCTG
 TCCATCCCCACATCCCCGTCTGTCCTGTGATTTGGATAAGAGCTTGTGTTCTT
 GAAAAAAA

FIGURE 122

MAVYVGMLRLGRLCAGSSGVILGARAALSRSWQEARLQGVRFLSSREVDRMVSTPIGGLSYVQ
 GCTKKHLNSKTVQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLLPDLTTVISVDAPLPGTLLDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTGS PKGATLSHYNIVNNSNILGERLKHEKTPEQLRMILPNPLY
 HCLGSVAGTMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPP E LIRAIINKINMKDLVVAYGTTENS PVTFAHF PEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNT P GELCIRGYCVM LGYWGE PQKTEEAVDQDKWYWTGDVAT
 MNEQGFCKIVGRSKDMII RGGENIYPAELEDFFH THPKVQE VQVGVKDDRMGEEICACIRL
 KDG EETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413**N-glycosylation Site:**

amino acids 282-285

FIGURE 123

CAACTCCAACATTTAGGAGAGCGCCTGAAACTGCATGAGAAGAACCCAGAGCAGTTGCGGA
TGATCCTGCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCG
ATGTACGGTGCCACCCCTCATCCTGGCTCTCCATCTCAATGGCAAGAAGGCAGTGGAGGC
CATCAGCAGAGAGAGAGGACCTTCTGTATGGTACCCCCACGATGTTCTGGACATTCTGA
ACCAGCCAGACTCTCAGTTATGACATCTCGACCATGTCGGAGGTGTCATTGCTGGTCC
CCTGCACCTCCAGAGTTGATCGAGCCATCATCAACAAGATAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCGTGACATTCGCGCACCTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCC**ATG**GACCCCCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTGCTTCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCC
 TGCAGAAAGCAGATGACGGATGCTCCCCAACAAAGATGAAGACAGTGAAGTGCGCGCCGGC
 GTGGACGTGCAACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGCC
 AGTGCGGGTTGCGGTTCTGGGACTCCCCGCAAGAATGACCGCGCCCTGGATCTTACGGGC
 TTCTGGCGTTCATCCAGTCAGCAATGCGCTCAGGATCGCTGCAACGCAAAGCTAACCTC
 ACCTCGGGCGCTCGACCCGGCAGGTAATGAGACTGCATACCCGCAAACGGCGTGGAGGT
 CTACAGCTGTGTTGGGCTGAGCCGGAGGCCTGCCAGGGTACATCGCCGCCGGTGTGAGCT
 GCTACAAACGCCAGCGATCATGTCATAAGGGCTGCTCGACGGCAACGTCACCTGACGGCA
 GCTAATGTGACTGTGTCCTTGCCCTGCCCCGGCTGTGTCAGGATGAATTCTGCACTCGGG
 TGGAGTAACAGGCCAGGGTTCACGCTCAGTGGCTCTGTTGCCAGGGTCCCCGTGTAACT
 CTGACCTCCGCAACAAGACCTACTTCTCCCCTGAAATCCCACCCCTTGTCCGGCTGCCCT
 CCAGAGGCCACGACTGTGGCCTCAACCACATCTGTCACCACCTTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACAAACCCATGCCAGGCCAACCGAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCCTCCGGATGAGGAGCCAGGTTGACTGGAGGCCGCTGCCACCCAGGAC
 CGCAGCAATTCAAGGGCAGTATCTGCAAAGGGGGCCCCCAGCAGCCCCATAATAAGGCTG
 TGTGGCTCCCACAGCTGGATTGGCAGCCCTCTGTTGGCGTGGCTGCTGGTGTCTACTGT
GAGCTTCTCCACCTGGAAATTCCCTCTCACCTACTTCTCTGGCCCTGGTACCCCTCTCT
 CATCACCTCTGTCCTCCACCACTGGACTGGGCTGGCCAGGCCCTGTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTGCGGCTTGGAAATAAAACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTGAGGACAGCTCCTGTATCCTCTCATCTTGTCTC
 TCCGCTGTCTCTTGATGTTAGGACAGAGTGAAGAGAAGTCAGCTGTCACGGGAAGGTG
 AGAGAGAGGATGCTAACTTCTACTCACCTTCTCTAGCCAGCCTGGACTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAACGACTGCCCTCCACTCCCGCATTTGGG
 GAATCGGTTCCCCATATGTCCTCTACTAGACTGTGAGGACTCTCGAGGGGGGCCGGTAC
 CCAATTCCGCCCCATAGTGAGTCGTA

1252660

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLRLGGAQALECYSCVQKADDGCSPKNMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFTIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCFDGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPFGTLSGCCQGSRCNSDLRNKTYFSPRIPLVLVRLLPPEPTT
VASTTSVTTSTSAPVRPTTCKMPAPTSQTPRQGVHEASRDEEPRLTGGAA GHQDRNSNG
QYPAKGGPQOPHNKGCVAPTAGLAALLLAVAAGVLL

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FIGURE 126

CGGGACTCGGCGGGTCCCTCCTGGAGTCGGAGGGACCGGCTGTGCAGACGCCATGGAGT
 TGGTGCTGGTCTTCCTCTGCAGCCTGCTGGCCCCATGGCCTGCCAGTGCAGCTGAAAAG
 GAGAAGGAAATGGACCCCTTTCATTATGATTACCAAGACCTGAGGATTGGGGACTGGTGT
 CGCTGTGGTCCCTCTCGGGATCCTCCTTACCTAAGTCGCAGGTGCAAGTGCAGTT
 TCAATCAGAACGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGTGGAGAACCTCATCACCGCC
 AATGCAACAGAGCCCCAGAACGAGAACACTGAAGTCAGCCATCAGGTGGAAGCCTCTGGAA
 CCTGAGGGCGCTGCTGAACCTTGGATGCAAATGTCGATGCTTAAAAAACCGGCCACTTC
 AGCAACAGCCCTTCCCCAGGAGAACCCAAGAACCTGTGTGTCCCCCACCTATCCCTCTA
 ACACCATTCCCTCCACCTGATGATGCAACTAACACTGCCCTCCCACTGCAGCCTGCCGTCC
 GCCCACCTCCCGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTGCTAACTGTG
 GTCTTGTGGCTACTTGTGATGGTATTGTGTTGTTAGTGAACGTGGACTCGCTT
 CCCAGGGAGGGCGTAGGCCACATGGCCATCTGCTCTCCCTGCCCGTGGCCCTCCATCAC
 CTTCTGCTCTAGGAGGCTGCTGTGCCCAGAACAGCCCCCTCCCTGATTAGGATGC
 GTAGGGTAAGAGCACGGGCAGTGGCTTCAGTCGCTTGGGACCTGGGAAGGTTGCGACAC
 TTTGTATCATTCTCATGGACTCCTTCACTCCTTAACAAAACCTGCTTCTTATCCC
 ACCTGATCCCAGTCTGAAGGTCTTAGCAACTGGAGATAACAAGCAAGGAGCTGGTGAGCC
 CAGCGTTGACGTCAGCAGGCTATGCCCTCCGTGGTTAATTCTCCAGGGGCTCCACG
 AGGAGTCCCACATCTGCCCGCCCTCAAGAGGCCGGGGATCCAGGCCAGGGCTCT
 ACTCTGCCCTGGGAATGTGTCCCCCTGCATATCTTCAGCAATAACTCCATGGGCTCTGG
 GACCCCTACCCCTTCAACCTCCCTGAGACTCAATCTACAGCCCAGCTCATCCAG
 ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGAATAGTTGAAGGACTCCCTGTTCC
 GTTGGGCCAGCACACCGGATGGATGGAGGGAGAGCAGAGGCCCTTGCTTCTGCCTACG
 TCCCCTAGATGGGAGCAGAGGCAACTCCCGCATCTTGCTGCCTGTCGGTGGTCA
 GCGGTGAGCAGGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTGGGAACAGTGAGAG
 GTTGAAGGTATAACAGAGACTGGGAACTCAACCCAGATCCGCCCTCCTGCTCTGTGTT
 CCCCGGAAACCAACCAACCGTGGCTGTGACCCATTGCTGTTCTGTATCGTGTATCTA
 CCTCAACAAACAGAAAAAGGAATAAAATCTTGTGTTCT

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSGILLILSRRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTEVQPSGGSLWNLRRLLPEPLDANVDA

FIGURE 128

AAACTTGACGCCATGAAGATCCGGTCCTCCTGCCGTGGTGCCTCTGCCCCCTGGTGCT
CCACTCTGCCAGGGAGCCACCCCTGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTAACACCCCTTCAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTGAACGGCACGCCCTTTGAGTCATAAAAGGAAACTCCCTT
CCTCAACTGGGATGCCCTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
GACCATGACCTCCACTGGAAGAGGGGCTAGCGTGAGCGCTGATTCTAACCTACCATAACT
CTTCCCTGCCTCAGGAACTCCAATAAACATTCCATCCAAA

FIGURE 129

MKIPVLPAAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSAFKADE
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

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FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTAGGGAATACAAACCAGCC**ATGGGGGTGGAGATTGC**
CTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTT
TTCTCCAGCCAGTTCCAACTCAGGAGACAGGTCCAAGGCCATGGGAGATCTCCCTGTGGC
TTTGCAGGCCACTCA**TGA**GAGTGTTTGTGTAAGTATTTAGAATACTGTTGACTTCT
TCATGATTAATAACCATCCTTGCAGTTTATGAGGCTTAGGGGAATGTCAACCTCA
AATTTTGTATTAACGATGGCTTCATTACCCACCACTATTTAAGGTCCCTTATTTT
AGGTTCAAGGTTCATTGACTTGAGAAAAGTGCCCTCTGCAGCTCATTGATTGTTATC
TTCACTATTAATTGTAACGATTAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCTGACACATTATGTAAGTGATCCCACAAATGTGATTGTTAATTAAA
TGTTATTCTAATATTAGTACATTCACTGATGTAATATGAATAACCAGAAATCTATTCTT
AAAAGTTTGAGTATATTTCAACTAGATATTGTATAGAAAGACTGAATAGTGATG

FIGURE 131

MGVEIAFASVILTCLSLLAAGVSQVILLQPVPTQETGPKAMGDLSCGFAGHS

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCG**ATG**GAGTGGTGGCTAGCTGCCGCTCGGCCTCG
 GCTGCTGTTCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTATTGACCAAATTAAACAGGTCTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCAGGTGTATAGAAGAGGATCTAACCTCTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAAGCTAGGGACCCACTATCAGATCACTAAGAAC
 GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGAGTGGTGTGAGCAGCTTATT
 TTGGAAAGTGTGGCGCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCTAAATGGATGGAGGCCTGCCATCCCAGTCTCTCCCTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCTGCTGGACATTGGAGGGGGACCTGCTGTTGGCCAATTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTCAGAGAAAGATCTGTAAGGTAGCAGCACAGTG
 GCCATGGAAAAAGAAAAACTCTACAGCATATTCCGAGGATCAAGGACAAGTCAGAACGAG
 ATCCTCTCATTCTCTGTCTCGGAAAAACCCAAAATGTTGATGCAAGAACACACCAAAAC
 CAGGCTGGAAATCTGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCATCTTGT
 GGATCACTGCAAATACAAGTATCTGTTAATTTCGAGGCGTAGCTGCAAGTTCGGTTTA
 AACACCTCTCCTGTGCGCTCACTGTTCCATGTTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTCACTATATCCAGTCAAAACAGATCTCCATGTCCA
 AGAGCTGTTACAATTGTAAGCAATGATGATGATGCTCAAGAGATTGCTGAAAGGGAA
 GCCAGTTATTAGGAACCATTGCGATGGATGACATCACCTGTTACTGGGAGAACCTCTG
 AGTGAATACTCTAAATTCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCCAAATGTTGAAAATGAACT**TAG**TAGTCATAGGACCATAGTCCTCTTGTGGCA
 ACAGATCTCAGATATCTACGGTGAGAAGCTTACCATAGCTGGCTCTATAACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTAAAATGTGCTAATACACTGATATGAAGCGATTCAACCTTTGGATGAAATAAGGA
 CCAGAAAATCGTGAGATGTTGAAACCCACTCTACCTTCAAGGCAACT
 ACAGCTGTGCGCTCAGATCATCCACCTGATGAGTCCATCACTGTAATTGACTGTGTC
 TGTGATGATGCCCTTGTCCATTATTGGAGCAGAAAATTGCTACTGGAAAGTAGTACAA
 CTCATTGCTGAAATTGTAACCGCTGATCTCTGTCACCTTATTAAATGTTAGG
 AAACCCATGGGTTATGAAAATACTTGGGATCATCTGTAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGAGGAGTTCTTTGTAACACATAAACTGTTACTCAG
 GAGGTTCTATAATGCCACATAGAAGAGGCCATTGCTGAGTAATTGCAATTGGATT
 TCAGGTTCCCTTTGTCCTCATGCCACTTCTTAATGCCCTCTAAAGCCAAA

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FIGURE 133

MEWWASSPLRLWLLLFLPLSAQGRQKESGSKWKVFDQINRSLENYPECSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRLKGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYLFNFRGVAASFRFKHLFLCGSLVFHVGDEWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNLQMDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

FIGURE 134

CACCCCTCATTCTCGCC**ATGGCCCTGCACTGTC**TCTGATCCCCTGCCTCT
TCATCCTGGCTTGGCACGGAGTGGAGTCGGCTTACCTCCCTGGGCCACTTCTT
GGAGGGATCCGGAGTCTGGTGGCTGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
CCGCAGCATCTTGCCCCCTGGCATGGATCTGGGCTCTGCTTATTTGTGGGCAGC
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCGGTACTTGGGCTCTTCAG
AGGTCACTGTATGTGGCTGCACTGCCCTGGCTTGAGCTGGTATGCGGTACTGGGAGCC
CATACCCAAAGGCCCTGTGGGGAGGCTGGGCTGAGCCATGGCACCTGGTGCCGC
TCCTCTGCTTGTGCTCATGTCATCTCTGGCTCTCATCTTAGCATCCTCTGCTT
GACTATGCTGAGCTCATGGCCTAAACAGGTATACTACCATGTCGCTGGGCTGGCGAGCC
TCTGGCCCTGAAGTCTCCCGGGCTCTAGACTCTTCCCACCTGCGCCACCCAGTGTGTG
TGGAGCTGTCGACAGTGCTGGGTGGCTACCCGGCACGGACCGTCTCTCTTGCT
TTCTCTTACCCCTACTGGGCTGGCTACGGGCTGATCAGCAAGACCTCCCTACCT
CCGGGCCCAGTACAAGAAAATCCACCTGCTCTCGGCCCCAGGATGGGAGGAGAGT
GAGGAGCTACTCTGGTACAAGCCCTGTTCTCTCTCCACTGAATTCTAAATCTTAAC
ATCCAGGCCCTGGCTCTCATGCCAGAGGCCAATCCATGGACTGAAGGAGATGCCCTT
CTACTACTTGAGACTTTATCTGGGCTCAGCTCCATACCCCTAAATTCTGAGTTCTAGCCA
CTGAACCTCCAAGGCTCACCTCTCACAGCAAGGAAGGAGTGGGTATGGAAGTCATCTGTCCC
TTCACTGTTAGAGCATGACACTCTCCCTCAACAGCCTCTGAGAAGGAAGGATCTGCC
CTGACCACCTCCCTGGCACTGTTACTTGCCCTGCGCCTCAGGGTCCCTCTGCACCGCT
GGCTCCACTCCAAGAAGGTTGACAGGGCTGCAAGTCAACGGTCTAGCTCTGCACCTCTTAGGCCCT
GGCCCCAACCTGGCTCACCAACTCCGGCCCTAGTCTCTGCACCTCTTAGGCCCTGCC
GGGCTCAGACCCCAACCTAGTCAGGGGATTCTCTGCTCTTAACTCGATGACTTGGGCTC
CTGCTCTCCGAGGAAGATGCTCTGCAAGGGAAAATAAAAGTCAGCCCTTTCTA
AAAAAAAAAA

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FIGURE 135

MAPALLIPIAALASFILAFTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSLMAAERVKAWSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVVISWLLIFSILLVFDYAEMLGLKQVYYHVLGLGEPLALKSP
RALRLFSLRHPVCVELLTVLWVVP TLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

100-112-123-268-60

FIGURE 136

CCGAGCACAGGAGATTGCCCTGGCTTACGGGTGGCTGCCTGTGGAAAAGCTATCAAGGA
AGAAATTGCCAACCATGTCTTTTTCTGTTTCAGAGTAGTTCAACACAGATCTGAGTGT
TTAATTAAAGCATGGAATACAGAAAACAACAAAAACTTAAGCTTAATTTCATCTGGAATT
CCACAGTTTCTTAGCTCCTGGACCCGGTGACCTGTTGGCTCTCCCGCTGGCTGCTCTA
TCACGTGGTCTCCGACTACTCACCCGAGGTGAAAGAACCTCCGGCTCGGTGCTCTG
AGCTGCTGTGG**ATGG**CCTGGCTCTGGACTGTCCGAGTAGGATGTCACTGAGATCC
CTCAAATGGAGCCTCTGCTGTCACTCCTGAGTTCTTGTGATGTGGTACCTCAGGCC
TCCCCACTACAATGTGATAGAACCGGTGAACGGATGACTTCTATGAGTATGAGCGATT
ACAGACAAGACTTCACTCACACTCGAGAGCATTCAAACGTCTCATCAAATCATT
CTGGTCATTCTGGTGCACCCCCACCCCTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
TTGGGGTGAAGAAAAGTCTGGTGGGATATGAGGTTCTTACATTTCATTAGGCCAAG
AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCTAGAGGATGAAACACCTTCTTATGGT
GACATAATCGACAAGATTTCAGACACATATAAACTGACCTGAAAACCATTATGGC
ATTCAAGGGTGGTAACTGAGTTTGCCTTCAAGCAAGTACGTAATGAAGACAGACACTGATG
TTTCATCAACTGCAATTAGTGAAGTATCTTAAACCTAAACACTCAGAGAAGTTT
TTCACAGGTTATCCTTAATTGATAATTTCCTATAGAGGATTTACAAAAAACCATAT
TTCTTACCGAGGATTCCTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTATATAA
TGTCCAGAGATTGGTCCAAGGATCTATGAAATGATGGTCACGTAACCTTCAAGGTT
GAAGATGTTATGTCGGATCTTGAATTATAAAAGTGAAACATTATTCAGAGAAGA
CACAAATCTTCTTCTATAGAATCCATTGGATGTCACAGACGTGATTG
CAGCCCAGGGTTCTTCAAGGAGATCATCACTTTGGCAGGTGATGTAAGGAACACC
ACATGCCATTAT**TAAC**TTCACATTCTACAAAAAGCTAGAAGGACAGGATACCTTGTGAAA
GTGTTAAATAAAAGTAGTACTGTGGAAAATTCATGGGGAGGTGAGTGTGCTGGCTTACACTG
AACTGAAACTCATGAAAACCCAGACTGGAGACTGGAGGTTACACTTGTGATTATTAGTC
AGGCCCTCAAGATGATATGTGGAGAATTAAATAAAAGGATGGAGGTTTGTCAA
GAATTAAATAGGACCAACAAATTGGACATGTCATTCTGAGACTAGAATTCTTAAAGGG
TGTTACTGAGTTATAAGCTCACTAGGCTGAAAACAAACATGAGGTTTATTG
AACAAATGTAGTCACTTGAAGGTTTGTGATATCTTATGTGGATTACCAATTAAAAATATA
TGTAGTTCTGTGCAAAACTCTTCACTGAAGTTACTGAAACAAATTACCTGTGTTT
TGGTCATTATAAAAGTACTTCAAGATGTTGAGTATTTCAGTTATTATTTAAATTAA
CTTCAACTTGTGTTTAAATGTTGAGATTCAATACAAGATAAAAGGATAGTGAAT
CATTCTTACATGCAAACATTCCAGTTACTTAAGTCACTGAGTTATTGATACATCAC
TCCATTAAATGTAAGTCAGGTCAATTGCAATACAGTAATCTTGGACTTGTAAA
ATTTACTGTGGAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQD
FHFTLREHSNC SHQNPLVILVTSHPSDVKARQAIRVTWGEKKSSWG YEVLTFFLLG QEAEK
EDKMLA LSLDEHLLYGDII RQDFLDTYNNLT LKTI MAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYCSGLGYIMSRD
LVPRIYEMMGHVVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNNTCHY

FIGURE 138

CCTCTGTCACGTCTCGTGAAGACAAGATGAAGTTCACAATTGCTTTGCTGGACTTCTT
GGAGTCTTCTAGCTCTGCCCTAGCTAACTATAATCAACGTCATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAAATGAACACAATGTGGCCATGTTGACA
ATAACAAACGGATGGGACTCTGGAATTCCATCTGGGATTATGGAAATGGCTTGCTGCAACC
AGACTCTTCAAAGAAGACATGCATTGTCACAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTGATGCACTGGTCAGGAAAAAGAACGTTCAAGGGTAAGGGACCAGGAGGACAC
CTCCCAAGGGCCTGATGTAACAGTCACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCGTGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGAGCATT
CCTTCTGTTGGAGACACGGTGGAGAACTAAACAATTTTAAAGCCATATGGATTAGTCAT
CTGAATATGCTGTCAGAAAAAAATGGGCTCCAGTGGTTTACCATGTCATTCTGAAATT
TTCTCTACTAGTTATGTTGATTCTTAAGTTCAATAAAATCATTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQQSVVNNEHNVANVDNNNGWDSWNS
IWDYGNGFAATRLFQKKTCIVHKMNKEVMPSTIQSLDALVKEKKLQGKGPGGPPKGMLYSVN
PNKVDDLSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

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FIGURE 140

CATTTCTGAAACTAATCGTGTAGAATTGACTTGAAAAGCATTGCTTTACAGAAGTATA
 TTAACTTTTAGGAGTAATTCTAGTTGGATTGTAATATGAAATAATTAAAAGGGCTTCG
 CTCATATAGGAAAATCGCATATGGCTCTAGTATTAATTCTTATTGCTTACTGATTTTT
 TGAGTTAAGAGTTGTTATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAA
 GAATAAAAGTAGATTGAGTCTCCAATTATGTAAGCTCAGAAGAACTGGTTGTTACATG
 CAAGCTTATAGTTGAAATATTTCAGGAATTAC**ATG**AATGACAGTCTTCGAACCAATGTGT
 TTGTTCGATTTCAACCAGAGACTATAGCATGTGCTTCATCTACCTTGCAAGCTAGAGCACTT
 CAGATTCGGTGCACACTGTCCCCATTGGTTCTCTTTGGTACTACAGAAAGAGGAAAT
 CCAGGAAATCTGCATAGAAAACACTTAGGCTTATACCAGAAAAAGCCAAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTAAAAGCAAAGGGAA
 TTGAATCCGGATGGAACTCCAGCCCCATTCAACCCCTGGGTGGATTTCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATACCAATCTCATTATGTGAAGACAG
 TCAAAAAGAACCTGAGGATAGACACAGGCTCCTAACAGGCCCTTACAATGGTGAAGAAAAA
 GACAGCAAGAGAAGTAGAAAATAGCAGAAGTGCAGTCGATCGAGGTCAAGAACACGATCAG
 TTCTAGATCACATACTCCAAGAACAGACTATAATAATAGCGGGAGTCGATCTGAAACATACA
 GCTCGAGATCAAGAACAGGTCCCCAGTCAGTGAAGGCCCTCGAAGACATCATAATCAT
 GGTTCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTAAAAAGTCTAACAGACATGG
 TCATAAAAAGGAAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAAACACAGGCATGAAAGGGACATCATAGGGACAGGGCTGAACGATCTCGCTCCTT
 GAGAGGCTCCATAAAAGCAAGCACCAGTGGCAGTCGCTCAGGACATGGCAGGCACAGGGC
CTGACTTTCTTCTTGTGAGCCTGCATCAGTTCTGGTTTGCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAAAGCAGACTGATTAGGATTGATTCTTGAACCCCTCTA
 GGTCTCTAGAACACTGAGGACAGTTCTTGTGAAAGAACATATGTTAATTGGCACATT
 AAAATGCCCTAGCAGTATCTAATTAAAACATGGTCAGGTTCAATTGTAATTAGT
 TGTGTTATTGCTATAAGAACAGTCAGGAGCCTGAATTCTGTTAAAGAACATATGTTAATT
 ATACAGATAAAATTGCAAGACACTGTTCTATTAAAGTGTGTTATTGTTAAATGATGGTGAAT
 ACTTTCTAACACTGGTTGTCATGTGTAAGGATTTTACAAGGAAATAAAATACAAAT
 CTTGTTTTCTAAAAAAAAAAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSRSHSESPRHHNHGSPHLKAKHTRDDLKSSNRHGHRKKSRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRGHGRHRR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGTTATCA
TTTTTGAAANNTATCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTACAGAAATATAT
TANCTTTTAGAGTAATTCTAGTTGGATTGTAATATGAAATTATTTAAAAGGGCTCGCT
CATATATAGGAAAATCGCATATGGCCTAGTATTAATTNTTATGCTTACTGATTTTTG
AGTTAAGAGTTTATATGNTAGAATATGAGGATGTAAGATAAAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTGTAGCTTCAGAAGAACTGGTTGTTACATGCA
AGCTTATAGTTGAAATATTTTCAGGAATTACATGAATGACAGTCTCGAACCAATGTGTT
GTTCGATTCAACCAGAGANTATAGCATGTGCTTCATCTACCTGCAGNTAGAGCACTTC
GATTCCGTTGCCAACTNGTCCCATTGGTTCTCTTTGGTACTACAGAAGAGGAATCC
AGGAAATNTGCATAGAACACTTAGGCTTATACAGAAAAAGCCAAACTATGAATTACTG
AAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAACGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAACTCCAGCCCTTCAACCCTGGGTGGATTTCTCC

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FIGURE 143

GGCACGAGGCCTCGTCCAAGCTTGGCACGAGGGTGCACCGCGTCTCGCACGCGTC**ATGGC**
 GGTCTCGGAGTACAGCTGGTGGTGAACCTGCTACTGCCACCCATGCCACAGGCTGGCGC
 CACACTGCTCCTCGCGCTGGCTCTGTAACGGCAGTTGTTCCGATAACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCAATGGCCTAGTGAGGAGAACGGACTGTCTGCCCCGAGATGCCCGTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGCTCTGCGCTTCCCTGGAGTACAGTGG
 TTTGTGAACTTGTGTACTCGGGCGCGTGTACCTCTCACAGAGGCCACTACTACAT
 GCTGGGACCAGCAAGGAGACTAACATTGCTGTGTTCTGGTGCTGCTCACGGTGACCTTC
 CCATCAAGATGTCCTGACAGTGACACGGCTGTACTTCAGCGCCAGGAGGGGGTGGAGCGC
 TCTGTCTGCCACCTTGCCTCTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
 GGAGGAGACCCCTCGAGCTGGGCTGGAGCTGGCTGGCCAGCATGACCCAGAACTTAGAGC
 CACTTCTGAAGAACGAGGGCTGGGACTGGGCGCTCTGTGGCCAAGCTGGTATCCGCGT
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCACCTTCCCAGGCCCTGCCGCTGGC
 CCAGACCCACCGGGACGCACTGACCATGTCGGAGGACAGACCCATGCTGCAGTCCCTGCG
 ACACCACTTCCCTGTCCTCCCTGTTCATCTGTGGCTCTGGACAAAGCCATTGCAACGGGAC
 TTCTGCAACAGCCCGTTGGGAGACCCGTTCTCCCTGTCCTGCCATTGCGATTCTGCC
 CTCTGGCGCCTCTGGTGCTGGTGGCTGTGCTGCTGCCCTGCCGCTGGCGGTGACCCGGCC
 ACCTGCAAGGCCACCTGAAATCAGCAGGGTGGTCCGAGTCACTGCTATGTGACCGTGGT
 CGCATGCAAGGCCGTGAAATCAGCAGGGTGGTCCGAGTCACTGCTATGTGACCGTGGT
 GAGCTTGCACTGACGCCCTCATCCTCACCTCAACTGCAACTTCTGCTCAAGACGC
 TGGGAGGCTATTCCCTGGGCCCTGGGCCAGCTCTACTATCCCCGACCCATCCCTCAGCC
 AGCGCTGCCCATCGCTCTGGGAGGACGAAGTCCAGCAGACTGCAAGCGGGATTGCC
 GGCCCTGGTGGCCTGCTTACTCCCTCTCCGTGGCGTCTGGCCTACCTCATGGT
 GGACGGCTGCCAGCTGCTGCCAGCCTTTCGGCTCTACTTCCACCAAGCAGCTGGCA
 GGCTCC**TAG**CTGCCCTGCAAGCCCTCTGGGGCCCTGAGGTCTGTTCTGGGCCAGCGGGACA
 CTAGCCTGCCCTCTGTTGCGCCCCCTGTCCTGAGCTGCAAGGTGGGCCGGACTCCCC
 GCGCTTCCCTCACCAAGTGCCTGACCCGCGGCCCTTGGACGCCAGTTCTGCC
 GAACTGTCTCCTGGGCCAGCAGCATGAGGGTCCGAGGCCATTGCTCCGAAGCGTATG
 TGCCAGGTTGAGTGGCGAGGGTGTGCTGGCTGCTTCTGAACAAATAAGGAGCATGCC
 GATTTTAA

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FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEELRALAGKPRPRGRKE
RWANGLSEEKPPLSVPRDAPFQLETCPPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAAY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGWDWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMIQLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSSLSDSA
FDSGRILWLLVVVLCLLRAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLQYLTPLIILTNCCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLAGS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCAC
CCTCATGCACAGGCTGGGCCACACTGCTCCTCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATAACAAGCACCGTNTGAGGAGGAGCTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCC
GAGATGCCCGTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGCTCGCG
TTCTTCTGGAGTACCACTGGTTGTGGACTTTGCTGTACTCGGGCGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTCCTCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCATACCTCTCATCTGAGAATCAGAGAGCATAATCTTCTACGGGCCGTGATTATAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAATTCTTGTATCTACTGATTGTGGGGCATGGCAAGGTTGGCTTAAGGAGC
 TTGGCTGGTTGGGCCCTGTAGCTGACAGAAGGTTGGCCAGGGAGAACGACAGCACACTGCTCGGAGA**ATGAGG**
 CECTCTGTGCTGCTTGCCTGCTAGCTCTAACTCATGCAATGTGGCACCCGCACCTGCACCTTCTG
 TATTAGAACACTCTGAAAGGTTGGCTCCCAACTGACCAAAAGATAGGAAGAGGGCTCACAAAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCAAGGGTTCTGAGCTGCCACCATCTCTAA
 TGACAGACGAGCTGGCTAGACACCCCTGGCTACGTGCTCCGTGGCAGAGGGCAGGCCAAATCAGCCA
 GTGGACTCTGGCCGGAGCAACCGAACAGTGGGCCAGGGCTTGTAGAGATCCACTATTAGAGGCAAGTATTAA
 AAAAATAAATCAGACTTGTGAGCTTCTGAGGACAAGAGCCGGAGTGACTTGCACATTGCGAACATGGCAGG
 GCAGGGAAATTCTGAAAACACCATGGCCCTGAGCTGGCTTCCAACTGATGGCTAGGAGATGGTGA
 ATTACAGACATCAAGATCAATCAGAGTATGGCTTCCAACTGAGCTGGCTTCCAACTGAGCTGGTGA
 CCCACTGGTCCATATCATATTACCAACACATTATCTGATGGGTGATGCCAGAGACGCCCTACTGGCAG
 GAGACATCATTCAAAAGGTCACGGGATGACATGCCATAGCTCCCTACAACTACGCTGTGCTCTCTGG
 CAGCCCTGCCAGGTGCTGGCTGACTGTGATGGCTGAGACAGAGTGGCCAGGAAACATGGACAGGGCC
 GGATGGACTCTAGAGGAGGAGCAACGGAGACTGGCCAGGGCTTGTAGAGATCCACTATTAGAGGCAAGTATTAA
 TAAACTGGTGGCAAGGGTGGATGAGGCCCTGGGTTTCATCTCAATGTGCTGGATGGCGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGGCCATCAATGCAATGATCTCGATATGGCACCCAGGAAAG
 TGCGGCTCATCTGATTAGCGGAGTGAAGAGCTGTTGGCTGCTGGTGTCCGCCAGGTGCTGCCAGGGGCC
 CTGAGATCTTCAAGGAAGGCCAGGAGCAACAGATGGCAGCTGGTCCCAAGGGCAGGGAGAGGAGCAACACT
 CCCAACGGCTCATCTCAAACTTGTGATGAGAAGGTTGAAATATCCAAAAGAACCCCCGGTGAATCTCT
 CGGCATGACCGTGGCAAGGGGAGCATCACATAGAAATTGGGATTGGCTTATCTATGTCATCAGTGTGAGGCCG
 GAGGAGTCATAAGCAGAGTGGAAATAAAACAGGTGACATTITGGTGAATGTGGATGGGTGCAACTGACA
 GAGGTGAGCCGGAGTGGCCAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTGGAAAGT
 CAAAGACTATGAGGCCAGGAGACTGCAGCAGCCCAGCAGCCCTGGACTCCARACACATGGCCCCACCA
 GTGACTGTCCCCATCTGGCTCATGTGGCTGAATTACACGGCTGCTGTATAACTGTAAAGAATGTGATTA
 CGAAAGAACACAGCTGGAAAGTCTGGCTTCTGCAATTGAGGAGTTAGAAGATCAATGGAAACAAACCTT
 TTTCATCAATCCATTGTAAGGAAACACAGGATACATGAGATGACATCTGGCCAGGAGACTGTGAAAGRACT
 CTGCAATGGTAGAAAGTACATCAGGAATGACATCTGGCCAGGAGACTGTGAAAGRACTAAAGGAAGA
 ATTACTCTAATATTGTTCTGGCTGGCACTTTTA**TAG**AATCAATGATGGTCAGAGGAAACAGAAAAA
 TCACAAATAGGCTAAAGAGTTGAAACACTATATTATCTTGTGAGTTTTTATTTAAAGAAAGAATACATTGT
 AAAAATGTCAGGAAAGATGATCATCTAAAGGCAAGTACACTCAGAAATATGATTCACAAAAAATTA
 AAAACTACTGTTTTCTGAGTGTGGAGGATTCTCATTACTCTACAAACATTGTTTATATTTTCTATTCAAT
 AAAAGCCCTAAACAACTAAATGATTGTTGATACCCCACTGAATTCAAGCTGATTAAATTAAAGCTAAATTTTAA
 GTGATCTGCTGAAAGTCTGCCAGGGTACATTATGGCCATTTTAATTACAGCTAAATATTTTAAATGCA
 TTGCTGAGAACAGTGTGTTCTCATCAAACAGAAATAATTTTCAAGAAGTAA

FIGURE 147

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDGCA SLTAT
APSPEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGRSNRTRARPFERSTIRSR
FKKINRALSVLRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMRQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESA AHLI QASERRVHLVVSRQVRQRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVN IQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDRGRIKTGDILLNDGVELTEVS RSEAVALLKRTSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRC GDILLAVNGRSTSGMIHA CLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGTCAATTGAAAAAGAGATATCCACATCTTCAGGCCATATAAGGATAGAAGCT
GCACAGGGCAGCTTACTTACTCCAGCACCTCCTCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGGGTTTTAACATCATCAGCCCAGCAACAATGGTGGC
AATGTTCAAGGAGACAGTGACAATTGATAATGAAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTACACAAATTGGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTATCCTGAAGATGGACCATCAGAACATCCCTCCTGAACAAAT
CTCCAATGGTACATCTATGAGAACAGGCTCTGGACAACATGTTCTCCAACAAATCACCTG
GGTCAAGTACAACCCCTCTGGAGTCTGTGATCAAAGACGTGGATTGGTTCTGCTTGGTCAC
CCATTGAGAAAACTCTGCAAACATATCCTTGTATAAGGGGGAGTGGTGAAAACACACAT
AATGTCGGTGTGGAGGCTGTGCAAAGGCTGGCCTGGGCATCTGGGAATTCAATCTG
TGCAGACATTGTTTAGGATGATTAGCCCTTGTATCTTCAAAGAAATACATCC
TTGGTTACACTCAAAGTCAAATTAAATTCTTCCAATGCCCAACTAATTGAGATTC
AGTCAGAAAATATAATGCTGTATTATA

FIGURE 149

MKILVAFLVVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSSRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWKYNPLE
SLIKDWDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

FIGURE 150

GCCACGAGCCAGGAACTAGGAGGTTCTCACTGCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCATTGCCCTACAAAGTCTGGAAGTTTCCCCAAAG
 GCCGCTGGGTGTCATAACCTGCTGTGACCCCCAGCCACCACCGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCAAGAAGGTGGTGAAGACCCACGAGCCGGCTCCTT
 CAACCTCAACGTCAACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCTCCT
 CCACCTCAGGTGCCATGTGGACAGTGCAGGCTCACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGGGGCCAACCTCACTCTGCAAGGACAGAGGGCAGGCCAGGGTGGA
 GATGATGCCAGCGCTCTCGGGCAGCCCACCTATCACCAACAGCCTGATGGGAAGGATG
 GGCAGGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACCTCTCCCTGCCG
 AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCAGCACAGC
 CCTCACAGTGGTCCCCCAGGTGGTGACCAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
 GCCCCATCTTGCCCTGCCGCTCACAGGAGCACCCCGCTCTGAGTGAAGAGGAGTTGGG
 GGGTTCAGGATAGGAATGGGAGGTCAAGAGGACGCAAAGCAGCAGCCATG**TAGAATGAACC**
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTCACTGTTGTATTGGA
 GTTCATGCAAAATGAGTGTGTTAGCTGCTCTGCCACAAAAAAA

09992521.11401

FIGURE 151

MGLPGLFCLAVLAASSFKA
REEEITPVVSIAYKVL
EVFPKGRWLITCCAPOPPPPITYSL
CGTKNIKVAKKVVKT
HEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGVHLQQR
PCHRQPANFSFLP
SQTSDFWFCQA
ANNANVQHSALTVVPPGGDQKMEDWQGP
LESPILALPLYRSTRRLSEEEFG
GFRIGNGEV
RGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

C04711-120251-1114

FIGURE 152

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCTCTCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCCGGCTGGCGAGCCGACCCACTCTCTTGTCTATGACATCACCGT
 CATCCCTAAGTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTTCTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTCCCCTGGGAAGAAA
 CTAATGTCACAAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCACTGAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGAGATCTCCTCCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGGTGTGGCCATGTCTTCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTGTATGGGATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCTCAGGCACAACCCAACTCAGGGCCAC
 AGCCACCAACCCCTCATCCTTGCTGCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
 TCTGAGGAGAGTCCTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCTGTGAGCACG
 GTCTTGATCAAACCTGCCCTCTGTCTGGCAGCTGCCACGACCTACGGTGTATGTCAGT
 GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTATTCACTGCCTGATTCTT
 TTGCCAACATTACAGCAGTTACCTAACATATTATGCAATTTCCTTGGTGTAC
 TGATGGAATTCTGCACTTAAAGTCTGGCTGACTAAACAAGATATATCATTCTTCTTC
 TCTTTTTGGAAATCAAGTACTCTTGAATGATGATCTCTTCTTGCAAATGATATT
 GTCAGAAAATAATCACGTTAGACTTCAGACCTCTGGGATTCTTCCGTCTGAAAGAG
 AATTAAATTATTAATAAGAAAAAATTATTAATGATTGTTCTTAAAGTAATTAT
 TGTTCTGACTGATATTAAATAAGAGTTCTATTCCAAAAA

0311111202666

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRDPHSLCYDITVIPKFRPGPRWCAVQQQVDEKTFI
HYDCGNKTVPVSPLGKKLNVTAWKAQNPNLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTWHPGARKMKEKWENDKVVAMSFHYS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLLICCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTCGAAAACCCATCTATACAAACTATATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAAATTCTATTCTGACTTCAGTTATACCGTGGA**ATGGAG**
TTGATCCAACCATAACATCGTGGAGGGTTTAATTGGTAGCCCTCACCAATTCTG
GTGTGGCTTCTTGCAAGGAGTCACCTCAAATCATGAACCTGGCTGTTGATCAAAA
GAGAATTGGATTCTACTCTAAAGTCATAGGACTTGCACAAAGAACGCTAGCAGAAC
TCAACCTGGCCTCCCATAAACAGGACAGATTTCAGGTGATGCCAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAATCTCAAATTGGAGGCCAAC
CCACAGAACAGCATTCTGGGCAGGCTG**TAA**TCAAATTGTCGTACATGCTAACAGC
ATTGCTTTCCCCAAAATTAAACACATTGTGGAGAAGTGTGATGACTCTCCCTTACCTT
CCTCTCCATTCAAGCATTCAAAGTATATTTCATGAATTAAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTACCAATGAGAGAAAAAAATGCATTCCCTGTAT
CATCCTTTCAATAACTGTATTGAAAAAAAAAAAAAAAAAAAAAA

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHELWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRDYSGDGKNGFYINGGYESHEQIPKRKLKGQQPTEQHFWARL

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FIGURE 156

GTTCTCTTCCGAGGCAAAATCCCAGGCATGGTGAATTATGAAACGTGCCACACC**ATGAAG**
 CTCTTGCGAGGTAACTGTGACCAACACACTGGATTCGCATCCTGCTCCCGCTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTCAGGCATCGCTGCTGCCGCTCAGCCGGGCCCC
 AGAACCTGCCCTCCCGTTGCTCGTCAACCGATTCAAGGCTGGTGTGACAGCGCCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCGACACCTTCCGCCACCTCCACACCTGGAGGTCTGCAGT
 TGGGCAGGAACCTCCATCGGAGATTGAGGTGGGGCTTAACGGGCTGGCCAGCCTCAAC
 ACCCTGGAGCTTCCGACAACACTGGCTGACAGTCATCCCTAGCGGGGCTTGAATACCTGTC
 CAAGCTCGGGAGGCTCGCTCGAACACCCCATCGAAACATCCCTCTTACCGCTTC
 ACCGGGTGCCCTCCCTATGCGCTGGACTTGGGGAGCTCAAGAACGCTGGAGTATATCTCT
 GAGGGAGCTTGTGGGGCTTCAACCTCAAGTATCTGAACCTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTACACCCCTGGTGGGGCTGGAGAGATGTCAGGGAACACT
 TCCCTGAGATCAGGCCCTGGCTCTTCCATGGCCTGAGCTCCCTCAAGAACGCTCTGGGTATG
 AACCTCACAGGTAGCCGAACTGGGAAATGCTTGGCGGGCTGGCTCACTTGTGGAAC
 CAACATTGGCCCAAAATACTCTCTTGGCCCATGACCTTACCCGCTGGAGTACCG
 TGGTGGAGTTGCATCTACACCAACCCCTGGAACACTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCCAATTCCACCTGCTGTGGCCGTGTATGCTCCCAT
 GCACATGGCAGGGCCCTACCTGTGGAGGTGACAGGGCTCTTCCAGTGGCTGTGCCCCCT
 TCATCATGGACGCACCTCGAGAACCTCAACATTCTGAGGGCTGGATGGCAGAACACTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCAATGGGACAGTGCTCAGCACGC
 CTCCGCCCAAAAGATCTCTCTCAACGAGCCACCTTGAACATTTCACCTGCTGCTG
 TTTCAGACACTGGGGTGTACACATGCTGGTACCAATGTTGAGGGCAACTCCAACGCCCC
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCAACTACAGCTTCAACACAGT
 AACAGTGGAGACCAACGGAGATCTGCCCTGAGGACACAACGCAAAGTACAAGCTGTGCTCTA
 CCACGTTCACTGGTACCGCCGCAATATACCACTCTACCAACGGTGTCTTACAGACTACC
 CGTGTGCCAAGCAGGGCAGTACCGCCGACAGAACCCACTTGACAAGATGCGAGCACGCC
 GGATGAAGTCATGAAGACCAAGATCATCATTGGCTGTTTGCTGGAGTGACTCTGCTAG
 CTGCCGCAATGGTGTGATTTCTCTATAAAACTCTGTAAGGCCACAGCAGCGGAGTACAGTC
 ACAGCCGGGGACTGGTGGAGATAATCCAGGTGGACAGAACATCCACAGCAACATCCG
 AGCAGCAACAGCAGCTCCGTCGGTGTACGGTGGAGGGCAGTAGTGCTGCCACAAATT
 ATGACCATATAACTACAACACCTACAAACCCAGCACATGGGGCCACTGGACAGAAAAACAGC
 CTGGGGAACTCTGCAACCCCAAGTCACCACTATCTGTAACCTTATAATTAGACACCA
 TACCAAGGACAAGGTACAGGAAACTCAAATA**TGAC**CTCCCTCCCCAAAAAAACTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTGTACAGAGTGGGAGAGACTTTTCTTGT
 TATGCTTATATATAAGTCATGGGTGGTTAAAAAAACAGATTATATAAAATTAAAGA
 CAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILPFVYLTAQVWILCAAIAAAAASAGPQNCPSVCSCSNQFSKVVC
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDGLELKKLEY
ISEGAFEGLFNLKYLNLCMCNIKDMPNLTPLVGLEELMSGNHFPEIRPGSFHGLSSLKKLW
VMNSQVSLSIERNADFGLASLVELNLAHNNLSSLPHDLFTPRLYLVELHLHNPNWNCDCDILW
LAWWLREYIPTNSTCCGRCHA PMHMGRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLPGTVLSHASRHPRISVLNDT LNFSHVLLSDTGVTMCVTNVAGNSN
ASAYLNVSTAELNTSNYSFFTTVTVETTEISPEDTRKYKPVPTSTGYQPAYTTSTTVLIQ
TTRVPKQAVPATDTDKMQTSLDEVMKTTKIIIGCFVAVTLLAAMLIVFYKLRKRHQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEAGAVLPTIHDHINYNTYPAHGAHWTE
NSLGNSLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 158

FIGURE 159

MELGCWTQLGLTFLQQLLISLPLREYT VINEACPGAEWNIMCRECCEYDQIECVCPGKREVV
GYTI PCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIITKRVCGNERPAPIQSISGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSNEKRTCQQNGEWSKGQPICIKACREP KISDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLQSAPTKKPALPF GDLPMGYQHLHTQLQYECISPFYRRLGSSRTCLRTGK
WSGRAPSCIPICGKIENITA PKTQGLRWPWQAAIYRTSGVHD GSLHKGAWFLVC SGALVNE
RTVVVAAHCVTDLGKV TMK TADLKVV LGKFYRDDRDEKTIQSLQISAIILHPNYDILL
ADIAILKLLDKARISTRVQPI CLAASRDLSTS FQESHITVAGWNVLADVRSPGFKN DTLRSG
VVS VVD SLLCEEQHEDHGIPVSVTDNMFCASWEPTAPS DICTAETGGIAAVSF PGRASPEPR
WHLMGLVWSWSYDKTCSHRLSTAFTKVL PFKD WIERNMK

FIGURE 160

ACCAGGCATTGTATCTCAGTTGTCATCAAGTTCGCAATCAGATGGAAAAGCTCAACTTGA
 AGCTTTCTGCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAAC**ATGGC**
 TTCAACCTGACTTCCACCTTCCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCC
 GACAGTGGTTGGTGGGCCACCAGTAACACTACTTCGTTGCCCCATTCAAGAGATCTAAAG
 CAAAGGAGTTCATGGCTAATTCCATAAGACCCCATTTGGGAAGGGAAAACACTCTGACT
 AATGAAGCATCCACAGAAGTAGAACTTGACAACACTGTCCTCTGTGTCCTCCTAACCTCAG
 AGGCCAGAGCAAGCTCATTTCAAACCGATCTCAGTTGAAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGATGCCCTCAGGAATGTAAGCTTACAGAGGTGCGCATC
 CTCGTTCCCCACCGAACAGAGAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGATTATGGCATCTACGTCATCCACCAAGGCTGAAGGTAAGA
 TTAATCGAGCAAACCTTGAATGTTGGCTATCTAGAACCCCTCAAGGAAGAAAATTGGAC
 TGCTTATATTCCACGATGTTGGACCTGGTACCCGAGAATGACTTTAACCTTACAAGTGTGA
 GGAGCATCCAAGCATCTGGTGGTGGCAGGAACAGCACTGGTACAGGTTACAGTTACAGTG
 GATATTTGGGGGTGTACTGCCCTAAGCAGAGAGCAGTTCAAGGTGAATGGATTCTCT
 AACAAACTACTGGGGATGGGGAGGCAGAGACGATGACCTCAGACTCAGGGTTGAGCTCAAAG
 AATGAAAATTCCCGCCCCCTGCTGAAGTGGTAAATATACATGGCTTCCACACTAGAG
 ACAAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTTACACCAAGTGTACAGGAGCTGG
 AGAACAGATGGGTTGAGTAGTTGTTATAAATTAGTATCTGTGGAACACAATCCTTATA
 TATCAACATCACAGTGGATTCTGGTTGGCA**TGA**CCCTGGATCTTGGTGTGTTGG
 AAGAACTGATTCTTGGTGTCAATAATTGGCTAGAGACTTCAAATAGTAGCACACACATTA
 AGAACCTGTTACAGCTCATGGTAGCTGAATTTCCTTTGTATTTCTAGCAGAGCT
 CCTGGTAGTAGAGTATAAACAGTTGAACAAAGACAGCTTCTAGTCATTGATCATG
 AGGGTTAAATTGTAATATGGATACTGAAGGACTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTGAGGACTCTGGTTGAAGGGAGTTATTAAATTGAAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAAGACTGCTGAATGTCAGAGAGAACCCAGAGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCACTTACGTCACATCATCT
 GTGAAGTGGTGGTCAAGGTAGAGAGGCGTCACAAAAGAGGGAGAAAAGGGCAGCAATCA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGCTGCAAGGCAG
 CAGTAGCTGAGCTGGTGCAGGTGCTGATAGCCTCAGGGAGGACCTGCCAGGTATGCT
 TCCAGTGTACGCCCACCAAGAGAATACATTCTATTAGTTAAAGAGTTTGTAAAATGA
 TTTGTACAAGTAGGATATGAATTAGCAGTTACAAGTTACATATTAACATAATAAAA
 TGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAA

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FIGURE 161

MGFNLTFHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGYRQPQECKALQRV
A1LVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALK
WDCF1FHDVDLVPENDNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTA
LSREQFFKVNGFSNNYWGWWGGEDEDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDG
NEVNAERMKLLHQVSRVWRTDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

E02941 Y25Z6660

FIGURE 162

CGTGGGCCGGGTCGCGCAGCGGGCTGTGGGCAGCCCGAGGAGCGACCGCCAGTTCTC
 GAGCTCCAGCTGCATTCCTCCGCGTCCGCCAACGCTCTCCCGCTCCGGCCGA**ATG**
 GCCCAGGCAGTCTGGTCGGCCCTCGGCCGCATCTCTGGCTTGCTGCCTCCCTGGC
 CCCGGCAGGGTGGCCGCAGGCCTGTATGAACTCATCTCACCAACCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCACCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCACCTTACCGCTTCACTGGATCCACACCCCGTGGTGCCTACTGGCAA
 GATGGAGAAGGGTCTCACTCCACCCATCCGGTGTGGTCGGCCACGTGCCCCGGGAATTCCC
 TCTCTGCTGGGTCACTGCCGTGACTCTGGATGTGGCAGCGTGTGGCAGGGCTTGTG
 GTCTCCCATCACAGAGTCTCTGTGGGGACCTGTGTGTCACCCAGAACACTCCCTACC
 CTGGCCAGCTCTATCTCACTAACAGCCCTGTCTTCTCACTAACGGGATCTGGGACGGGACCCAG
 GCAACTTCTCAAGAGCCCTGTCTTCTCACTAACGGGATCTGGGACGGGACCCAGATG
 GTGACTGAAGACTCTGGTCTATTAACTACTTCCATCATGGGACCTTCACCTGAAGCT
 CAAACTGGTGGCGAGTGGGAAGAGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCTCTGTGAAGCTGCAGGAAACCCCTCGAGGGCATCCAAGTGTGGG
 CCCACCTTAATCAGACCTTCAAGGCTGAGTGCCTCCGCTGGAGGAAGGGGAGTGCACC
 TCTGACTGTGTGGCGTCTCAAGGCTGAGTGCCTCCGCTGGAGGAAGGGGAGTGCACC
 CTGTGTCCGTGGCCAGCACAGCTAACACCTGACCCACACCTCAAGGACCCCTGGGACTAC
 TGCTTCAGCATGGGCCAGGAATAATCATCAGCAAGACACATCAGTACACAAAGATCAGG
 GTGGCCCTCCAGAATCTAGCCGGTGTCTTGTCTTCCATGTGTCACACTTATCACTGTG
 TGTTGGCCTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGTTGGAG
 AACCCGGAGCCACCTCTGGGTCAAGTGTCTGCCAGATGTGCTGTGGCCTTCTTGTG
 GGAGACTCATGTGAAATTGTCTGTGAGAACACAGGGCTGCTCCGCCCTCT
 ATAAGTGTCAAACACTACACCGT**TGAG**ACTCCCCCTCCCCACCCATCTAGTGTAA
 CTGACTGCTGACTGGAGTTCCAGCAGGGTGTGTCACCACTGACCAAGGAGGGTTCATT
 TGCCTGGGGCTGTGGCTGATCATCCATCTGTACAGTTCAGCCACTGCCAACAGCC
 CCTCCCTCTGTGACCCCTGACCCGGCATTCAACCATCTGACAGTCCAGGACTGACA
 TAAGCCCCACTCGGTTACCAACCCCTTGACCCCTACCTTGAAAGAGGCTCGCAGGACT
 TTGATGCTGGGGTGTCTGGTGTGACTCTAGGGCTGGCTGCCCCACTGCCATTCTC
 CTCATATGGCACATCTGCTGTCTGGGTTCTAGTTCTCCCCACAGGCCCTAC
 CTGTGCCAGAGACTAGAAAAGGTCTAAAGGTTAAAATCCATAACTAAAGGTTGAC
 ACATAGATGGGACACTCACAGAGAGAAGTGTGACATGACACACCCACACACACA
 CACACACACAGAAAATACACATGGGCTACATGGGCTTACAGTGTGACGCTGT
 TCTGGTTAGTCGGTGTGGGATGCACCTGCACTAGAGCTGAAAGGAATTGACCTCA
 AGCAGCCCTGACAGGTCTGGGCGGGCCCTCCCTTGTGTTGTCTGCAAGTTCTGC
 GCCCTTATAAGGCCATCCTAGTCCCTGCGCAGGGGCTGGATGGGGCAGGACT
 AATACTGAGTGTGAGCTGGCTTATAAAATATACCTTATTATTCAGAACCCATCTGT
 AAACATTCACTGAGGAAAAGGCCCTGCACGGTAGAAGAGGTTGAGTCAGGCCGG
 TGGCTCACGCTGTAACTCCAGCATTGGGAGGCCAGGCGGGTGGATCACGAGATCAGGA
 GATCGAGACCAACCCCTGGCTAACACGGTAACACGGGACTTACTAAAAAAATACAAAAGTT
 AGCCGGCGTGGTGGGTGCTGTAGTCCAGCTACGGGAGGCTGAGGCAGGAGAATG
 GTGCGAACCCGGGAGGCCAGTGCAGTGAGCCAGATGGCCACTGCACTCCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTSATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPPSSYLTKTVLKVSFLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTLNFLGSPLTVCWRLKPECLPLEEGERHPVSVASTAYNLTHFRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFACATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCQMCQGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**CACTGAGCTCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTCCCA
CAACAGACGGGACA**CTTG**CAGAGCTGCAACCCCAGGACAGAGCTGGAGCCAGGCCAGCTG
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCC**ATCTGC**ATTTCTGCT
GCGGCTGCTGT**CATCGATCAA**AGTGTGGATGTGCTGCAAGACG**TAGA**ACCTACCTGCCCTG
CCCCCGTCCCCCTCCCTCTTATTATTCTGCTGCCAGAACATAGGTCTTGAATAAAA
TGGCTGGTTCTTTGTTTCCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCCTGCAATTGTTCTTGGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCACC**A**TGTTCTGTTGCTGCCCTTGTAGCCTGATTGTCACCTCTGGC
 ATCTCCCTGACTGTCCTCTCACCCCTCTCGTTTATCATCATAGTGCAGGCATTTTG
 AGTCTCCCTTGGTATCCGAAACACTACATGAAAGATCTGTTAAAATCTTGCCTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAACGACCAAGCTTACAAGCCCTACACCAAC
 GGAATCATGCAAAGGATCCCACACTCACTAGAAGAGATCAAAGAGATTGCTGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTGACATTTCTACTTTG
 GGAAAGGAATGGAGAACATTATGGATGAGGTGACAAAGAGATTCTCAGCAGAAACTG
 GAGTCCTGGAACCTGCTGAGCAGAACCAATTATAACTTCAGTACATCAGCCTCGGCTAC
 GGTCTGTGGGGTTAGGAGTGTGATTCGGTACTGCTTCTGCTGCCCTCAGGATAGCAC
 TGGCTTACACGGGATTAGCCTCTGGTGGGACAATCTGTTGGGAACTTGC
 GGGAGGTTAAAGGAAATGCTGAGTAAATGTTCACTTAATGTTACCGGATCTCGGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAACAGACAAAGAAATGGTGC
 ATCTGTGCAATCATACCTCACCGATGATGTATCTTGGCAGCGATGGCTATTG
 ATGGTGGTCAAGTCAGCAGGGGACTCATGGGTGATTGAGAGGACATGGTGAAGGCTG
 CCCACAGCTGTTGAGGCTCGGAAGTCAGGATGCCACCTGGTGGCTAAGGAGACTGA
 CTGAACATGTGAAGATAAAAGCAAGCTGCCATCTCTCATCTCCAGAAAGGACCTGC
 ATCAATAATACATCGGTGATGTTCAAAAGGGAAAGTTGAAATTGGAGCCACAGTTACCC
 TGGTCTATCAAGTATGACCTCAATTGCGATGCCCTTCGACAAAGCAGCAGAAATACGGG
 TGGTACGTAACCTGCTGCAATGATGACAGCTGGGCATTGTCGACGGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGAGCATGAAAGATGCTGCCAGTTGCAATAGGGTGAATCTG
 CATTGCAAGGAGGGAGGACTGTGACCTGCTGTGGGATGGGGCTGAAGAGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGGAGCAGCAAGAAGCTACAGCAAGATGATGTC
 GGGGAAACCACAAAGGAGCGCGCT**TGA**GCTGCCCTCAGCTGGCTGGGGC
 ACCGTGCGGGGTCGAA
 CGGGCTCAGAGCTGGATTGGCGCCGGCCCCACTGCTGTGCTCTTCCAGACTCCAGGG
 CTCCCCGGCTGCTCTGGATCCCAGGACTCCGGCTTCTGCCAGCGCAGCGGATCCCTGT
 GCACCCGGCGCAGCTACCCCTGGTGGTCAAACCGATGCTGCTGGGTGTTGCA
 CGAGATGCTTCTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAAC
 CCTTGCACGCTGTGGGCTGAGTGGTGGGGAGATGTCGGCATGGTCTTGT
 AGAGATGGCGGTTACAAGAGTCTGTTATGCAAGCCCTGTCGGAGGGATGTC
 GGGGGGGGGCCACCCGCTCTCCAGGAAAGGACAGCTGAGGCACTGTGGCT
 CGGCTTCCGCTCAACATGCC
 CTTGGACCTCTGCAAGACATGAGAAGGAAACTGTCATCTGCAGGGGGCTTCA
 CGCAGGAAATG
 AAGGGTTAGATTTTATGCTGCTGATGGGGTTACTAAAGGGAGGGAAAGAGG
 CAGGTG
 GGCGCTGACTGGGCATGGGGAGAACGTTGTTGACTCCAGGCTAACCTGA
 ACTCCCC
 ATGTGATGGCGCTTGTGAATGTTGCTCGGTTCCCATCTGTAATATGAGTC
 GGGGG
 GAATGGGGTGAATCCACCTCACAGGGCTGTTGGGGATTAAAGTGC
 TGGGGTGA
 AGGACACATCAGTCAGTGTCAAGTACAGGCCACAAAAGGGGGCA
 CGCGCAGGCTGAG
 CTCAGAGCTGTC
 GACTGGCTTGGATTGAGTAAATAACTGGCTGGTGA
 TGA

FIGURE 167

MFLLLFDLSIVNLLGISLTVLFTLLLVLIVPAIFGVSGIRKLYMKSLKIFAWATLRME
RGAKEKNHQLYKPYTNGITAKDPTSLEEEIKEIRRGSSKALDNTPEFELSDIFYFCRKGMETIMDDEVTKRFAEELSWNLLSRNTYNFQYISLRLTVLWGLGVLI
RYCFLPLRIALAFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRA
LTAIITYHDRENPRNGGICVANHTSPIDVIIASDGYYAMVGQVHGGLMGVIQRAMVKACPHVWF
ERSEVKDRHLVAKRLTEHVQDKSKLPILIFPEGTCINNTSVMMFKGSFEIGATVYPVAIKYDPQFGDAFWNS
SKYGMVTYL
LRMMTSAIVCSVWYLPPTMTRA
DEDADAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKD
TF
KEEQQKLYSKMIVGNHKDRSRS

167/330

FIGURE 168

GCCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCGCCCTCACCCGGACCCCTGGCCCTCA
 CGTCTCCCTCCAGGG**ATG**GCGCTGGCGCTTTGATGATGCCCTCGGCAGCCTGGCCTCCAC
 ACCTGGCAGGCCAGGGCTGTTCCCACCATCCTGCCCTGGGCTGGCTCAGACACCTTTGA
 CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCCACCATGCCCTGCTGCGGGATCCTGGAGGCAGGCCAGGAGACCTGGAGGAC
 AAGCGTCAGGGCTTACCTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCATTATGGT
 CTACACCAACTCATCGAACACCTTGACTGGGAGTTGAATCAGGGCGTGCAGGGCGGAG
 GCTCCCGGGAGCTACATGAGGCACCTTCCCTCAAGGCCCTGCTTACCTGATCCGG
 GCCCTGCAGCTGCTGGAGGCAGTGGGGCTGCAGCAGGGGACCTGGGAGGTGGTGTCCG
 AGGGTGTGGGAGCCTCGCTTGAACCCAAGAGGGCTGGGGACTCTGTCGCTGGCCAGT
 TTGCGCTCAGCTCCCTGGATAAGGCAGTGGCCACAGATTGGGAGAAAGAGGGGGCTGT
 GTGTCGCGCCAGGGTGAGCTAGGGTCACAATCTGAGGGGCTCTCTGCCCCCTG
 GAAGACTCTGCTTTGGCCCTGGAGAGTCCAGCTCAGGGTTGGGCC**TGA**AAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAAGCAAGAACATGGTCCGGACCCAGGCCCTAGCAGCCTCTCCCCAACAGG
 ATGTTGGCCTGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTATGTGATGGGACTTCC
 GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLKEEMAH
ALLRESWEAAQETWEDKRGRGLTPPPGFKAQNQGIAIMVYTNSSNTLYWELNQAVRTGGGSREL
YMRHFPFKALHFYLIRALQLLRGSGGCGSRGPGEVVFRGVGSLRFEPKRLGDSVRLQGFASSS
LDKVAHARFGEKRRGCVSAPGVQLGSQSEGASSLPPWKLILLAPGEFQLSGVG

FIGURE 170

GTGGCCTCATTCAGGGCTGACTTCCAGAGAGCAAT**ATGGCTGGTCCCCAACATGCC**TAC
 CCCTCATCTATATCCTTGGCAGCTCACAGGGTACGCAGCCTCTGGACCCGTGAAAGAGAGCTG
 GTCGGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCAAAGTAAGCAAGTTGACTC
 TATTGTCTGGACCTTCAACACAACCCCTTGTCAACCATAACGCCAGAAGGGGCACTATCA
 TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
 CTCAGCAAATCGAAGAAGATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
 CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGCTACAGCACCTGTCAAAGCCTAAAG
 TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGTCATG
 GAACATGGGAAGAGGATGTGATTTATACCTGGAGGGCCCTGGCAAGCAGCCAATGAGTC
 CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGTATGACCTTCATCT
 GCGTTGCCAGGAACCTGTCAAGCAGAAACTCTCAAGCCCCATCCTTGCAGGAAGCTGT
 GAAGGTGCTCCTGATGACCCAGATTCTCCATGGTCTCCTGTCTCTGTGTTGGTCCCCCT
 CCTGCTCAGTCTCTTGTACTGGGCTATTCTTGGTTCTGAAGAGAGAGAGACAAGAAG
 AGTACATTGAAGAGAAGAAGAGAGTGACATTGTGGAAACTCCTAACATATGCCCT
 TCTGGAGAGAACACAGAGTACGACACAATCCTCACACTAATAGAACAACTCTAAAGGAAGA
 TCCAGCAAATACGGTTACTCCACTGTGAAATACCGAAAAAGATGGAAAATCCCCACTCAC
 TGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTATC**TAGACAGCAGTG**
 CACTCCCCCTAACGTCTGCTCA

170/330 T252660

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSGVGAFTPLKSKVKQVDISIVWTFTNTPPLVT
IQPEGGTIIVTQNRRERVDFPDGGYSLKLSKLKKNDSGIYYVGIFYSSSLQQPSTQEYVLHV
YEHLSKPKVMTGQLQSNSKNGTCVTNLTCMHEGEDDVITYWKALGQAANESHNGSILPISWRW
GESDMTFIGVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLVPLLLSLFVGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRТИLKEDPANTVYSTVEIP
KKMENPHSLLTMDPTRLFAYENVI

FIGURE 172

CTGGTCCCCAACATGCCTCACCCCATCTATATCCTTGGCAGCTCACAGGTCAGCAGCC
TCTGGACCGTGAAAGAGCTGGTCGGTCCGGTGGTGGGGCCGTGACTTCCCCCTGAAGTC
CAAAGTAAGCAAGTTGACTCTATTGTCTGGACCTCAACACAACCCCTTGTACCCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAATCGAAGAAGATGACTCAGGGATCTACTATGT
GGGGATATAACAGCTCATCACTCCAGCAGGCCCTCACCCAGGACTACGTGCTGCATGCTACG
AGCACCTGTCAAGCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTTACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTGTGCCAGGAACCCCTGTCAAGCAGAAACTCTCAAGCCCC
ATCCTTGCCAGGAAGGTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCATGGTCTCCT
GTGTCTCCTGTTGGTGCCCCCTCTGCTCAGTCTCTTGACTGGGCTATTCCTTGGTTCT
TGAAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAGAGAGTGGACATTGTCGGGAA
ACTCCTAACATATGCCCTATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACATCTAAAGGAAGATCCAGCAAATCGTTACTCCACTGTGAAATACCGAAAA
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGTATTTGCTATGAG
AATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTGCTCAAAAAAAAAAAAAAA

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FIGURE 173

GGAAAGACGTGGTCTGACAGACAGACAATCCTATCCCTACAAAATGAAGATGCTGCTGCT
GCTGTGTTGGACTGACCTAGTCGTGTCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATAATGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGCCAATTAGCTTTCTGGACCAAATCCATGCTTGAGAAA
TTCTTAGTCTTAAAGTCATACTGTAAGAGATGAAGAGTGCCTCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTAATATTCTGTGACGTATGATGGATTCAATACATTACT
ATACCTAAGACAGACTATGATAACTTCTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGCTCTATGGCCGAGAACAGATTGAGTTGAGCTCAGACATCAAGGAA
GGTTTGACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCCTCAGGGCCGAGAATGAGAATGGCCTGAGCCTCCAGTGTGAGTTGAC
ACTTCTCACAGGACTCCACCATCATCCCTCTATCCATACAGCATCCCCAGTATAAATT
TGTGATCTGATTCATCCTGTCACTGAGAAGTCCAACTTCAAGTCTATCACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTAAATTCTCTTGATACACCCCTTGACAAT
TTTCATGAAATTATTCCTCTGTTCAATAATGATTACCTTGCACCTAA

FIGURE 174

MKMLLLCLGLTLVCVHAEEASSTGRNFNVEKINGEWTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLKVHTVRDEECSELSMVA DKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLS DIKERFAQLCEEHGILRENIIDL SNANRCLOARE

FIGURE 175

GGCTCGAGCGTTCTGAGCCAGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCA~~G~~CCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATA~~CC~~TCAATTG
TCAGCTTAGTTGAGGAAGACCAATTCTCAAAACCCATCTCTGCTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGTGCAACAAACAGAACAGA~~CT~~GGAA~~AT~~GTTCTTCATCATTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGATTGCATGCTGATATCCATCCAGGCTCTTAAAGGTCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGGAATTTCATTGAAAAACATCAGTGA
CATTCCATCCAGAATCCTCAACTTGCA~~G~~GTGGTTTCATGACTTTGTGCACCTCCTACTG
GTTTCAAAAACCCACCA~~G~~TAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTCAGGCTATTGCT
TGTTGGAATTCTGGAGGTCTGTTGGGCTCAGTCAGATAGTCATCGGTTCCGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTCTAGT~~TT~~AATGGGAATAAAATGTAAGTA
TCAGTAGTTGAAAAAAAAAA

FIGURE 176

MTCCEGWTSCNGFSLLVLLLGVVLNAPIPLIVSLVEEDQFSQNPI
SCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM
LISIQLALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDT
MASGWRASSFHFDSEENKHRL
IHFSVFGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCA**ATG**AGGCT
GTCAGTGTGTCCTGATGGCTCGCTGGCCCTTGCTGCTACCAGGCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTTGCAGCCAAGTTGGAAGTGAAAGCACTG
CACCGATCAGATATCTTTAAGAAACGACTCTATTGAAAAAGTCTGTTGGAA**AATAGT**GAA
AAAATGTGGTGTGTGACATGTAaaaATGCTCAACCTGGTTCAAAGTCTTCAACGACACC
CTGATCTCACTAAAAATTGTAAGGTTCAACACGTTGCTTAATAAATCACTGCCCTGC

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLOVAKLNPPPEALAALKLEV
KHCTDQISFKKRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGGCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GACCAGATCCGTGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACGTGAC**ATGG**GAGAGAGTGACCCCTGGCCCTTCCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTGCCAATAAGACGATCCCTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTCGGGAGGGCTCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTG
CAAATGCAAATAAGAGCAGCCAGAACGCAGCACAGTCCGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCT**TGA**GCACAGGACTGGCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTCTGATCAGGAGGCTTCTTATGAATTAAACTCG
CCCCACCAACCCCTCA

FIGURE 180

MERVTLALLLLAGLTAEANDPFANKDDPFYDWNKLQLSGLICGGLLAIAGIAAVLSGCKC
YKSSOKOHSPVPEKAIPPLITPGSATTC

FIGURE 181

GGAGAAGAGGTTGTGTCGGACAAGCTGCTCCCACAGAAGGATGTCGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGCCCCATGGCTACTCCTGCTGCTGGTTGTGGCCTC
 CTGGCTACTCGCCCGCATCCTGGCTGGACCTATGCCCTATAACAACTGCCGCCGGCTCC
 AGTGTTCACAGCCCCAAACGGA~~ACTGGTTTGGGT~~CACCTGGCCTGATCACTCCT
 ACAGAGGAGGGCTGAAGGACTCGACCCAGATGTCGGCACCTATTCCCAGGGCTTACGGT
 ATGGCTGGTCCCATCATCCCCCTCATGTTTATGCCACCTGACACCATCCGGTCTATCA
 CCAATGCCCTAGCTGCCATTGCAACCAAGGATAATCTCTCATCAGGTTCTGAAGGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGGCCACCGTGGATGTCAC
 GCCCGCCTCCATTCAACATCCTGAAGTCCTATAACGATCTCAACAAGAGTGC
 AACAA
 TCATGCTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTC
 TGACATGTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTGACAGGCCATTG
 TCAGGAGAGGCCACTGAAATATGGCACCATCTGGAGCTAGTGC
 CCCTTGAGAGAAAA
 GAAGCCAGCATATCCTCAGCACATGGACTTCTGATTACCTCTCCATGACGGGCGCGC
 TTCCACAGGGCCTGCCCTGGTCATGACTTCACAGACGCTGTC
 CATCCGGAGCGCGCTCG
 CACCCCTCCCCACTCAGGGTATTGATGATT
 TTTCAAAGACAAGCCAAGTCAAAGACTTTGG
 ATTTCATTGATGTGCTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTGGAGGCCATGACAC
 CAGGCCAGTGGCCTCTC
 CTGGGTCCTGTACAACCTTGCAGGGCACCCAGAAATACCA
 CAGGAGCGCTGCCAGCAGGAGGTG
 AAGAGCTCTGAAGGACCGCGATCTAAAGAGATTGAATGGGAC
 GACCTGCCAGCTGCC
 TTCCTGACCATGTGCGTGAAGGAGGCCAGTACATCCCCAGCT
 CCCCCTCATCTCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTC
 ATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGTCCATCACAACCCAACTGTG
 TGCGCCGATCCTGAGGTCTACGAC
 CCCTCCGCTTGACCCAGAGAACAGCAAGGGGAGGT
 CACCTCTGGTTTATTCTTCTC
 CGCAGGGGCCAGGA~~ACTG~~CATCGGGCAGGC
 GTTCCGCATGGCGAGATGAAAGTGGCCTGG
 CGTTGATGCTGCTGC
 ACTTCCGGTTCTGCCAGACCA
 CACTGAGGCCCGCAGGAAGCTGGAA
 TTGATCATGCGCGCCAGGGCGGGCTTGGCTGCCGGTGGAG
 CCCCCTGAATGTA
 GGCTTGCA
GTGACTTCTGACCCATCCACCTGTTTTGCA
 GATTGTCATGAATAAACGGTGCTGTCAA

FIGURE 182

MSLLSLPWGLRPVAMSPWLLLLLVVGSWLLARIILAWTYAFYNNCRRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDKSTQMSATYSQGFTVWLGPPIIPFIVLCHPDТИRSITNASAAIAPKDNLF
IRFLKPWLGEGILLSGGDKWSRHRRLTPAFHFNILKSYTIFNKSANIMLDKWQHЛАSEGS
SRLDMFEHISLMTLDSLQKCIFSFDHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRFRHACRLVHDFTDAVIRERRRTLPTQGIDDFFKDKAKSKTLDFIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRCQEVSQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCTGC
TGTTTGCTTTCACAGGATTCTTAAATCCTCTTATCTCTCCTGACTCCAGGGAA
AATATCCTTCACACTCTCAGCACCATGAAGACGCCGCTTAACCCGGAGGAGCTAGAAA
GAGCTCCCTTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTAACCCAAAGAGGAAATTGAGAAAGTTTCAAGGATT
CTCTGGACAAGATCCTAACATTTACTGAGTCATCTTGGCCAGAATCTGGAAACCATA
AGAAACGTGAGACTCCTGATTGCTTCTGAAATACTGTGTC**TGA**AGTGAATAAGCATCTG
TAGTCAGCTCAGAACACCCATCTAGAATATGAAAAATAACACAATGCTGATTGAAA
AGTGTGGAGAAAAACTAGGCCAAACTACACCCCTGTTATTGTTACCTGGAAAATAATCCTCT
ATGTTTGACAAAAAAAAAAAAAA

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

09992521.11402

FIGURE 185

GAACATTTAGTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAACTGCAGGCCACCTGCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCTGCTCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTCCTGAGCCCTGAACACCAGAGACTCCAGCAGAGAAAGGAGTCGAAGAACGCCACCA
GCCAAGCTGCAGCCCCGAGCTTAGCAGGCTGGCTCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACCTGGAAGTCCGGTTAACGCCCTTGATGTTGGAATCAAGCTGT
CAGGGGTTCACTTACAGCAGCACAGCCAGGCCCTGGGAAGTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCAGCCGACAAG**TGA**TGCCACAAGCCTTACTCACCTCTCT
AAGTTAGAAGCGCTCATCTGGCTTTCGCTTGCTCTGCAGCAACTCCACGACTGTTGTA
CAAGCTCAGGAGGCGATAATGTTCAAACGTGA

FIGURE 186

MPSPGTVCSSLGGMLWLDSLAMAGSSFLSPEHQRVQQRKESKKPAKLQPRALAGWLRPEDG
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATGCCATCCTGCTGTATGTCCTCGTCAGTACCTC
 GTGAACCCGGGGTGCCTCGCACGGACCCCAGATGTCAGAAATTGAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCGGTGCAAGGTGCAAGACCCCTGATAGTCGATCATGGGATGCTCGTG
 CTCCTGCTGGACTTCTGGCTTGGTGCACCTGGCCAGCTGCTCATCTCCACATCTACCT
 GAGTATGTCACCCACCTAACGCCCGATCCCCCAAGGCTGGTGGTCAAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCTAACCTGAGCCCCCACGCCCTGGGCCAGAGTCCTT
 GTCCCCCGTGTGCGATGTGTTCAAGGGTCAAGCTCTCCAGAAGTGAGATCATGGACAAAAA
 GGGCAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCAGACCTGCAAGGAGTGGTGCAGGTGCTTGAAGTAACAAGTTAAAATGTTCAAG
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAACTAGTAGAAATTCTAACATGAAATATATTACAGGGCAGGTCAACCACAA
 AACAACTGAAGCGAGAGCTGTGGTCTGGTCTCACAGTGGCAGCGGTAGGGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACAACCTCCCTGCTCTGGCACCCAGCGTTGGTCAAGTGGGCAAGCTGCAAAGCG
 TCTTCCATTCTCTGGCAGTGGTGGGCCAGGGCTGTGGCCTCTCAGGGGTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTGGCCA
 ACCCCCTGGTCAGGGCAGAGGGAGTTGGTGGGTAGGCTCTGGGCTCACCTCATCTCCAGA
 GCATCCCCCTGCCTGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA
 GCCTCCTTGTTCATAACCACAGGTACCCCTACAAACCAACTGTCCCCACACAACCTGGGAT
 GTTTAAACACACACCTCTAACGCATATCTTACAGTCAGTGTGCTTGCTGAGGGTTGA
 ATTTTTTAATGAAAGTGCATGAAAATCACTGGATTAAATCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDFLGLVHLGQLLIFHIYLSMSPTLSRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAEELTPRPAGVVPGA

FIGURE 189

GGAGTGCAGATGGCATCCTCGGTTCTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG
 ATGGAGCTCTCGAAGGCCCTCTGGCAGCGAACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTCTCCACAACATCCCTGCTCAGCAACTACTGGTTGTGGCACACAGAAGG
 TGCCCAGCCCCGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTGACATGCCAGTGTCCCTG
 GATGGAGATAACACATCCACCCAGGAGGTGTCAGAACATACAACACTGGGAGACTGGGATGA
 CCGGTTCCCTCCGGAGCTCCGGAGTGGCATGGCTATCTGTGAGGAAACTGTGGAGA
 AACCAGGGAGAGGTGGCAGATTCTATGAACTTACACCACAGCCAAGAGAGGGTGGAGAAA
 GGACTACTGGAATTGCCACGTTGCAAGGCCATGTCACCCACTCTCCGATTGGAGGGAA
 GCGGGTGTGGAGAAGGGCTCCCTCCCTCCCTGGGGCTTGTGGCAAAATCTA
 TGGTTATCCCTGGAAACGCACTACCTACATGGACTTCATTCACTCAGCTCCCTGCT
 ACTAACAGACTTGACTCACTGGGAACCCCTGCCTGTGGCTCAAACGTAGCGCCCTTGCTG
 CTGTTTCTCTGCTCTGTCAGTCTCTGGGATGGTGGCCACATGATGTATTCAAAAGTC
 TTCCAAGCGACTGTCACACTGGGTCAGAAGACTGGAGACCACATGTTGAAATTATGGCTG
 GGCCTTCTACATGGCTGGCTCTCCACCTGCTGCATGGCTGGCTGCAACCTTC
 ACACGTACACCAGGATGGTGTGGAGTTCAAGTGAAGCATAGTAAGAGCTCAAGGAAAAC
 CCGAAGCTGCTACCATCACCATCAGTGTTCCTCGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTGTGACCAGTACCAACAGTATCATAATCAGCCATCCACTCTGCTCTGAGG
 GAGTCGACTTCACTCCGAGCTGCGGAACAAGGGATTCAAAGAGGGGAGCCAGGAGCTG
 AAAGAACGAGTTAGGTATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGTTGGGA
 GTAGGCTGAGGCCACCTTACACGTCGTGATTATCAACATGTGTTAACCAACATCCG
 TCTCTTGAGCATGGTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTCTACAGCTCATCTGTTCACCCAC
 CCCACATCTCACACATCCAGAATTCCCTTTACTGATAGTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLILSAILSMMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDTNTSTQEVVQYNWETGDDRFSFRSGMWLSCETVEEPGERCRSFIETPPAKR
GEKGGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQI
PPATNRLATHWEPCILWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLETTCLE
LWLGLLHGALLHLLHVGCHHLQHVHQDGAGVQVQA

FIGURE 191

AACTGGAAAGGAAAGAAAAGGTCAGCTTGGCCAGATGTGGTTACCCCTGGTCTCCTG
 TCTTTATGTCTTCTCTCTTCTATTCTGTCACTCCCTCACTTAAGTCTCAGGCCTGTCA
 GCAGCTCTGTGGACATTGCCATCCCTCTGGTAGCAGCAGAACAGGACAACCTATG
 TTATGGATGTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCCTGTGCTTCTGT
 GATCTCTATGACAGAGCCACTTCTCCACCTCTGAATGTTCCCTGCTCTGAAATCTGGCATG
 AGATGGCACAGGTGACCGACGCAGAAGCCACCAGAACATCTTGCCCTGCCATTCCCTCCCAA
 GTCTGTTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCAATGGCATTACAGAGAAAG
 CAATCTGTGGCTAGTGGCAGATTACCATGCAAGCCCCCAGGAGAAATGGAGGAGCTTGT
 AGCCACCTCCCTGTCA GCCAGTATTAAACATGCCCCCTCCCCCTGCCCGCCGTAGATTCA
 GACATTGCCCTGTGTGCCACCAAACAGGACTTCCCCCTGGCTGGCATCCCTGGCTCT
 CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTCAGCTCCGTTACT
 ATGGCGATGGCCATGATGTTACAATCCCACCTGCGCTGAATAATCAAGTGGAAAGGGGAAGCA
 GAGGGAAATGGGGCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCCTGAGGAAAAACCAAA
 GGGAAAGCAACAGGAACCTCTGCAACTGGTTTTATCGAAAGATCATCCCTGCCGTGAGATGC
 TGTTGAAGGGGACAAGAAATGTAGCTGGAGAAGATTGTAGTGAAGATGCAGGTGTGAAGGAA
 ATAGAACAGTCTGCTGGAGTCAGACCTGGAATTCTGATTCCAACACTCTTATTACTTGGG
 AAGTCACTCAGCCTCCCGTAGCCATCTCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
 AACCCAAGGAAACTAACATGTAGGTACTAGTGAATACCCCAATGGTTCTCCAATTATGCC
 CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

FIGURE 192

MWLPPLGLLSLCLSPLPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGSGME
HRNHLCFCFDLYDRATSPPLKCSLL

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FIGURE 193

GTAGCCCCGCTTGGGCTCCCGCTGCCGCTGCGCCGCCGCCCTCGGCTGGAGGCCAGGAGCAGCTA
 CGCCCATGGCAGGCATCAAAAGCTTTGATTAGTTGTCCTTGGAGGAGCAATCGACTGATGTTTTGATGCTT
 GGATGTGCCCTTCCAATATAACAAAAATACTGGCCCTCTTGTCTTATTTTTACATCCTTCACCTAATTC
 ATACTGCATAGCAAGAAGATTAGTGATGATACAGATGCTAGAAGCAGCTGCAACTATACTAGGCTTTCTTGCTTGGGA
 TTACACAGGCATTGCGCTGAGCTTGGACTCCATTTGATTAGTATTGCCAGAGCACATCTGATGACTGGGA
 GCTTGCGACTTGTCTCACAGGAAACACAGTCATTTGCAACTATACTAGGCTTTCTTGCTTGGGA
 CAATGACGACTTCAGCTGGCAGCAGTGGCTGAAGAAGAAATTACAGTCAATTTGCAATGGACTCCGTGATT
 GTTGGCCATTCAAGGCACACAGGAGCTTGGAGATTAATGCTGAAGCTTGTGGGATTTA
 GGTGTCCTTCTACTTTTATGTAAGCATACTATTTCACAGAAGCTCTGCAAGGATTAAAAGGATTTTCT
 CTTTGAAAAGCTTGACTGATTTCACACTTATCTATAGTACTGTTTTGTGTTGCTGCTGTAATTAAATAT
 TTATGTTGTTGGCTTGTGATTGTTTGGAGATCAATGCAATTAAACACTTTTAAATGTAATCA
 TTTGATTGGTAGGAACTTCAGGATTCGGCCGCTCTTACAGGACTACATCTTCTCTAAATTATT
 TAGCCCTACATTAAACAAATAAATGTTTGGCTGAGCTGAGCTGAGATGACATCCTCCAAATGTTATG
 CAGACATACAGACGGTGGCATACGTGACTGATACACTGCAAAATAGCTGCAATTATGCTGCAATTACAG
 GGGCAACTGTTAATGCCCATGGCCCTCCGTTAAGGGTTGTGTTTACTGTAGACAGATGTTTGGGATTG
 AAAATTATTATGGATGCTCACCTGGAGGGTCTCTCTCTCTCAATTGTAAGGAAATTATGTTAACTTTA
 AGGTAAGGGTGTAAAACATTGAGATAAGGTTTTATTTATGTTTATATTGTTAGAGTGTGATGCAATGT
 GGGGAAGAAATGACATGAAATTCTTGGATCTCTTGTCTCTTGTCTTAACTGTAATTGTAATTGTTGCTCCTATC
 AACCTTCATGTTTACCTGTTAAATGGACATACATGGAAACACTACTGATGAGGGACAGTGTATGTTG
 ATCATATAGCCGAAAACCTTCCTCTCTCTCTTGTCTTGTCTTGTCTTAACTTACATACATGTTG
 TAACCTTTCAAATATGTTAAACACTTAGAGTGTCTTACTACCTGGAAAATAATTGCTATGCCGTACATT
 CAGAGTGGCCCTCCCTGCAAGGCTTGGCATGATTAACAAGTAACCTGTTAGCTTACAGATAATTCTGCA
 TTAACAGTTAAAGATTTAGGCTAACCTTAAGCCGACTGACTTTAGATGAGTTCTTAAAGGTATATCATGTTAATTAAAG
 TATTGTTAAAGACAAGTTCTGTATACCTGTTGACTCTTCAACTGTTTGTGTTTGTGTTTGTGTTTGTGTTT
 CCTTATAAAAGGCAATTGGCTGAGTAACTGCAAGTGGCTGAGACTTGGAGCTCAGCTATATAGCAGCTTCAAGAACAT
 ACGTACACAAAAAAATCCAGAACAGGCATGATCAATTATAGTGGCTGTTTACATCTAATAATTATCAGGA
 CTTTTTCAGGACTGGGTATAAAAACATTCAAGTTGGCTGACAGTTTTGTTAAGGATATTGTTGATG
 TTATACATACATACATACATAAAATATTGGCCCATCAGGCCAAACTCAGTAATCATGACAGCTGCTGTTG
 TTATGAAGTTTATTCAGAAGAAAATGGGAATAATTGGATTGTCAGCTTTTACTAAAGATGCTAA
 AGCCACAGGTTTATGGCTAACCTTAAGCCGACTGACTTTAGATGAGATGACGGGAAGCAGGAGCAAAATATCG
 GGTGAGGTACACATGAGTTAGAGAGCTGTTGAGACAGTTGGAAACTCTTGTCTTGTGATCTACTGGACTTT
 TTTTGGAGGAAGTGCATCTGGTCTCCCTATTCTGTTCTGGATGTCAGTGCAGTCATGCTACTG
 TTATACACTTGGCCACAGACTTTTCAACAGCTGCGTATTATTTCTATATACATAATTGCAATTGGCAGCATT
 GTGCTTGTGACCTGTATAACTGCTGACATAGTGTCTGCTGATTTCTAGGCTAGTTACTGGAGATAATGAT
 TTCCATAGAATATGCACTGATACACATGACATTCTCTATGGAAAGAAAATTGATGATGAAACAAATAA
 AGATTTAAATATCTATTAAAAAA

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTTGIVVSAFGLPIVFARAHLIEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

FIGURE 195

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQGFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNNTFRPPMNLRSVDSLNSYKLNQALAPDLFHGLRKLTLLHMRANAIQFVFPVRIFQDCRS
LKFLDIGYNQNLKSLARNFSAGLFKLTELHLEHNLDLVKVNFAHFPRLISLHSLCLRRRNKVAIV
VSSLWDVVNLKEKMDLSGNIEYMEPHVFTETVPHLQLSLOLDSNRLLTYIEPRILNWSWKSITSIT
LAGNLWDGCRNVCALASWLSNFQGRYDGNLQLCASPEYAQGEDVDLDAVYAFHLCEDGAEPPTSG
HLLSAVTNRSDLGPASSATTLAGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMAL
LIFSFLIVVVLVLYVSWKCFPASLRQLRCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCAGA**ATGGCGT**CCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
 GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTGAGCCAA
 CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCCGTTGAGTTCCCGCGACAAGATGG
 TGTCAGTCTGGTGCAAGAAGGTACGCCGTCTCAGACATGCTCCTGCCGTGGATGGGAA
 CTCGTCCTGGCTTCAGGAGCCGGATTGGCGTCTCAGACGTGGGCTCCACCTGGACTGTGG
 CGCGGGCGAACCTGCCGTCTCCGCCACTCTGACCGCTTCTGGCATGACCCGCACCTGT
 GGCGCTCTGGGACGAGGCACCTGGCTCTTCTCGTGGACGCCAGCGCGTGCCCTGCCGC
 CACGACGACGTCTTCTTCCCGCTAGTGCTCCTTCCCGCTGGGCTCGGCCCTGGCGTAG
 CCCCCTGCGTGTCCGCAGCATCTCGCTCTGGCCGGACGTTACGCGCGACGAGGACCTGG
 CTGTTTCTGGCGTCCCGCGCGGGCGCTACGCTTCCACGGGCCGGCGC**TGA**GCCTG
 GGCCCCGAGGACTGCGCGGACCCGTCGGCTGCGTCTGGCAACGCGGAGGCCAGCCGTG
 GATCTGCCGGCCCTGCTCAGCCCCCT

FIGURE 198

MGVILGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAEVFPAKVMVSVLVQE
GHAVSDMPLLPLDGELEVLAGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPLWRSRGDEA
PGLFFFDAERVPCRHHDDVFFPPSASFRVGLPGASPVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPAGLSVGPEDCADPSGCVCVGNAAQWPWICAALLQP

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FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTC**ATG**GGGACCAGTGAACAGCTGAAGCGAATGTT
TGAGCCTACTCGTTGATTGCAACTATCATGGTGCCTGTTGACTTACCCCTGTGTT
CTGCCTTTGGTGGCATAACAAAGGGACTTGCACTTATCTTCTGCATTTGCAGTCTTGGCA
TTGACGTGGTACAGCCTTCCTCATACCATTTGCAAGGGATGCTGTGAAGAAGTGTGTTG
CGTGTGCTTGCA**TAA**TTCATGGCAGTTTATGAAGCTTGGAAAGGCACATGGACAGAAG
CTGGTGGACAGTTTGTAACTATCTCGAAACCTCTGCTTACAGACATGTGCCTTTATCT
TGCAGCAATGTGTTGCTTGATTGCAACATTGAGGGTTACTTTGGAAGCAACAATACAT
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTGTGGAGTGGAA
TCTTCCTCATGTACCTGTTCCCTCTGGATGTTGCCACTGAATTCCCATGAATAACAAAC
CTATTCAAGCAACAGCAA
AAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWHNKGALIFCILQSLALTWYSLSFIP
FARDAVKKCFAVCLA

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FIGURE 201

TTGAGCGCAGGTGAGCTCTGCCGTTCCGGGGCGTCTCCAGTCACCCCTCCGCCGTACCCGCCGCGC
 CCGAGGGAGTCTCTCCAGACCCCTCCCTCCGGTGCCTCAAAACTAATACGGACTGAACGGATCCTGCGAGGGT
 GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGCAACTACCATCCATAAGCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTGAAGAATTTCTTGTTGCTCTCATACTTGCTGACTGAGTCTTC
 AACCAACCTTTCTCTCCAACAGACAGAGAAAGGCTACTAGTGTCTTGATGGATTCCGTTGGGATTACT
 TATATAAAACTTCCAACGCCCCATTTCATTATAATTATGAATATGGTCTCACGTGAACCAACTTAATGTT
 TTATTACAAAAACTACCTAACCTTAACTTGGTAACCTGGCTTCTTGCAGAGAAATCATGGGATTGTTGC
 AAATGATATGTTGATCCTATCGGAACAAAATCTTCTCTTGATCACAATGAAATTATGATTCACAGTT
 GGGAAAGCAGCACCAATATGGATCACAAACAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGCCCGGA
 ACAGATGTAaaaaATACATAGCCTTCCACTACATACATGGCTTCAATGAGTCAGTTCTGAGTAG
 ATGGCCAAAATTGTTGAATGTTACGTCAAAAGGCCATAATCTGGTCTTCTCTATTGGGAAGCCCT
 ATGACATGGCCACCATGGGACCTGACAGTCCGCTCATGGGCTGTCATTCAGATATGCAAGAAGTTA
 GGATATCTACATAAATGCTGAAAAGGCAAGTTGTGGAAACACTGACCTTAATCATCACAGTGTATGG
 ATAGCAGCATGCTCTGAGGAAGGGTATAGAACCTTGACAGTACTGGATAAAGGACCAACTAACCTGATTTG
 ATCAATCTCAGTAGCAGCATCTGCCAAGGAGTAAAGAGGTTATGAGAAGTCTATGAGACTAACCTGAGCT
 CATCCTAAATTACTGTTCACAAAAGAACGCTTCCAGAAAGTGGCATTACAATAACAGCTGGAATTCA
 ACCAATCATAGCAGTGGCTGATGAGGGTGCACATTTCAGATAACTGATCCTAAATTGTCAGTTCTGAGAAC
 ACGGTTACGATAATGCTTAGCAGATATGCTCCTAAATTGTCAGCTTACACTATGCCCACCTCTCAATATCA
 TCAAAGAACGACATGAACCTCACAGATTGTCACCTACTATGCCCACCTCTCAATATCACTGCATGCCACA
 CAATGATCATTCTGGAAATGCTCAGGATCTCTCAACGCAATGCCAAAGGGTGGTCCCTTACACAGAGTA
 CTATACCTCCTGGTAGTTGAAACAGGAGATAATGACCAAGGGGTGATACCTTACATAGGTC
 TCTCTGGCAGCATATAGTGTATTTTGTAATTTTCAATTAAAGCATTAAATTCACAGTCAAAATACCTGC
 CITACAAAGATATGCTGAAATAGCTCAACCTATTACAGCCTAAATGTTGACTTCAAGGTTCTGAGTGGATTTC
 TTGAACTGGAGATTCTCAATAATTGTCAGTTAAAGGTTCAARCTCTGGAAACAGTTCACAAACATCTGC
 AGAACCCATTAAAGCAGTACATATTAGGTATACACACACACACACACACACACAGGACCAAA
 AATACTACACTGCAAAGATAAAGATGTCAGACTATGTCCTCATTTGTCAGTACAGGATAGATAAG
 ATCTGCTTATTGGACTGGCCAGATAATGTAATATTAGCAACTTGGACTATGTAAGAAGTCCATTAT
 ATTGCACTTAAATTCTCTCTGATGGTACTTTAATTGAAATGCACTTATGGACAGTTAGTCTTATAAC
 TTGATTGAAATGACAATTGTCACCCAGTACAGAATACTGTTACGCAATTGTCAAACTGAAGGAAATT
 TCTAAATAATCCGAAATATGAAACATAGRAAACTATCTCCATAAAATTGAGAGAGAAGAGGTTGATAAGTGTGA
 AAATAAATGTAACCTTGAACCTTGAATTTCAGAGATGTTCCCAACAGCAGAAATGCAACTGTTG
 TTCTGTCCTTATTCTTCCAGAGAACGCTGGTTTCAATTATTGTTCTTCCCTCAAAAGAGAGTCAAAACTGACAG
 ATTGTTCTAAATATAATTGTTCTGTCATAAAATTATGTAATTCTCTATATGTTGCACTTACTGTT
 TAATAATGAGACACCATGAAATACATTCTCTATATGTTGCAATGGCTGAATAGAAGCAACCCAGCA
 CCATCTCAGCAATGTTCTTGTGTAATTATTGCTCTTGAAAATTAAATCACTTAACTACATTACATTAA
 AAATCAAATTGGATAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSDGFRWDYLYKVPPTPHFHYIMKYGVHVK
QVTNVFITKTPNHYTLVTGLFAENHGIVANDMFDPIRINKSFSLDHMNIYDSKFWEETPIW
ITNQRAGHTSGAAMWPGTDVKIHKRFPTHMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPIMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTYYKKEDVPERWHYKYN
SRIQPPIIAVADEGWHLQNKSDDFLGNHGYDNALADMHPIFLAHGPFRKNFSKEAMNSTD
LYPLLCHLLNITAMPNGSFWNVQDLNSAMPRVVPTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTGTGATCCCGATTCGCTCCCACGGGGGGACCTTTGTAAGTCGGGGAGGCCAG
 GACAGGCCACCCCTGGGGGGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCCTGCCTGGGTACACAGCCAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGAGGGCC
 AAGGTGGCTCCGCTGAGAGGATGACCAAGTCTTAAGGCACTTCACCGTCGTGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
 CCTGCCCTGGCCCCGACCCAGGGCCCCCTGACTTCAGGGCATGTTGAGGAAACTGTT
 CAGCTCCACAGGTTTCAGGTATCATCATCTGCTGGTGGATGCCCTCTGGTGC
 TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCGACAAGATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTGGTCTTTTATGATGGAGATCATTTAAATT
 ATTTGCTTCCGCTGAGTTCTTCAACCACAAGTTGAGATCCTGGATGCCGTCGTGGTGG
 TGGCTCATCCTGGACATTGCTCTCTGTTCCAGGAGCACCAGTTGAGGCTCTGGG
 CTGCTGATTCTGCTCCGGTGTGGGGTGGCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAGAACGGCACTCTAACAGATGAATGTACAATTGGCGCCA
 AGATTCAACACCTTGAGTTCACTGCTCTGAGAACCCCTGGACTGATGAGTTGCTGTATC
 AACCTGTAAGGAGAACGCTCTCCGGATGGCTATGGAATGAAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTAAAGTCTGGAGTAAATGTGCTGTGTACAGAACAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACAGAACCTGACAGTCAGTGGCAGTTA
 TCACCTCAGATTACAATCACACAGAGCATCTGCCCTGGTCAATCACAGAGAACAAAACC
 AAAATCTATAAAGATATTCTGAAAATATGACAGAAATTGACAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELIIDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLSSFTTSLRSWMPVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRLKQMNVQLAAKIQHLEFS
CSEKPLD

FIGURE 205

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHKKLRLVKILDKKNDGRIDAQEIMQSLDLGVKISEQQAEKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRNGI
NVLKIAPESAIKFMAYEQIKRVLVGSDQETLRIHERLVAGSLAGAIAQSSIYPMVEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

12526660

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATAACGCTGGAACCTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATATTGGCTTGGTATTCAGGGAGACACTCCATCACAGTCACACTGTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGTACAATGGCTGAAGGAAGGTGTTAGGCTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTAGGCTGGCAGACAGCAGTGTGTT
 GCTGATCAAGTGTAGTTGGCAATGCCCTTTCGGCTGAAAAACGTGCAACTCACAGATGCA
 TGGCACCTACAAATGTATATCATCACTCTAAAGGCAAGGGGAATGCTAACCTGAGTATA
 AAACCTGGAGCCTTCAGCATGCCGAAGTGAATGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCATGGTCCCCAGCCCACAGTGGTCTGGCATCCAAAGTTGACCA
 GGGAGCCAACCTCTCGGAAGTCTCCAATACCAGCTTGAGCTGAACCTGAGAAATGTGACCA
 TGAAGGTTCTGTCCTGCTCTACAATGTTACGATCAACACACATACTCCTGTATGATTGAA
 ATGACATTGCCAAAGCAACAGGGATATCAAAGTGTACAGAATCGGAGATCAAAGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTCTGTGTCTCTTCTTTGACATCAGCT
 GGGCACCTCTGCCCTCACCTGATGCTAAA**TAAT**TGTCCTGGCCACAAAAAG
 CATGCAAAGTCATTGTCACACAGGGATCTACAGAACTATTCCACCAACAGATGACCTAG
 TTTTATTTCTGGAGGAATGAATTGATCATATCTAGAAGTCTGGAGTGAGCAACAAAGGCA
 AGAAACAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAAGATAAATCTATCTCAA
 GACATATTAGAAGTGGAAAATAATTGATGTGAACTAGACAAGTGTGTTAAGAGTGTAAAG
 TAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCGTACCT
 GGGGAGTGGAGAGGACAGGATAGTGCATGTTCTGCTCTGAATTGTTAGTTATGTC
 TAATGTTGCTCTGAGGAAGGCCCTGAAAGTCTATCCAAACATATCCACATCTTATATTCCA
 CAAATTAGCTGTAGTATGTCACCTAACAGCAGCTGCTAATTGACTGCCACTCGCAACTCAGG
 GGCAGCTGCATTAGTAATGGGTCATGATTCACTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTCCAACTGACAAATGCCAAAGTGGAGAAAATGATCATAATTGATCATAA
 ACAGAGCAGTCGGGGACACCGATTATAAATAACTGAGCACCTTCTTTAAACAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 208

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVILGLVHEFKEGKDESEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTSEIIRR
SHLQLLNASKASLCVSSFFAISWALLPLSPYLMK

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FIGURE 209

GAATTTGTAGAAGACAGGGCGTTGCC **ATG** GCGGGCGTCTCTGGGCAGGTGTTGGCTCTGGT
 GCTGGTGGCCGCTCTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCTCCGCCGGCCTG
 AGCGGGTTCATGAGCCGACCTGGGCCAGCAGTTGCTACAGGAGATGAAGACCCCTTTCTT
 AATACTGAGTACCTGATGCCCTTCCTCAACCAGTGTGGATCCCTCTATTACCTCAC
 CTTGGCATGACAGATCTGACCTGGCTGTGCCCATCTGTAACTCTGCTATCATCTTCA
 CACTGATTGTTGGGAAGGCCCTGGAGAAGATATTGGGAAACGTAAGTTAGACTACTGC
 GAGTGGGGACGCAGCTCTGTGGATCTGCACATACCTGTGTTAGTTCCCTCCAGAACCCAT
 CTCCCCAGAGTGGGTGAGGACACGGCCTTCCCACCTGCCCTTCCTGCACTGTTT
 GCTTCCCTGTGGCCATCAGAGTCCCTCCCTGGACAGTCTGGAGAAAAGACAGAGGCTGGG
 GTTGGGAT**TGA**AGACCAAGACCCCATCTGAGCCCTCCTCAGCCCTGTACAGCTCCTACT
 GGCGATGGCTGAGCTCAGACCCCTCTGATTTCTGCCTTATTATCCAGGACAGTGTGGCAT
 GGTCTCACCGTGATAGGAATTTCACCTGTCATACAAGCTCAGTGAGTAAGACCCAGGGC
 AACAGTCTACCTTGTGGCGAACCCACTTCCAGCTCTGCTGCCCTCAGGAAGCCCC
 GGGCATGAAAGTGTGGCAGTGAGGGATGGACCTAGCAGTCCCTCTGGCCTAGCTT
 CCTCCTCTTATGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAGAGTGAAG
 AGTTTTGTAAACCTTCAAGTGCTGTTAGCTGCCGGGATTAGCACAGGAGACTCTACGCTCA
 CCCTCAGCAACCTTCTGCCAGCAGCTCTCTGCCTAACATCTCAGGCTCCAGCCCA
 GCCACCAATTACTGTGGCCTGATCTGACTATCATGGTGGCAGGTCCATGGACTGCAGAACT
 CCAGCTGCATGGAAAGGGCAGCTGCAGACTTGTGGCAGAAATGCAAACGGAGGCCTCTG
 GGACTCAGTCAGAGCGTTGGCTGAATGAGGGGTGAACCGAGGGAAAGAGGTGCGTCGGA
 GTGGCAGATGCAGGAAATGAGCTGCTATTAGCCTGCTGCCACCCATGAGGTAGGCAG
 AAATCCTCACTGCCAGCCCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACTGAC
 TCCAGCACCTGGCAGTAGTAGCTGTCAATAATCTATGTAACAGACAAAAAA
 AAA

FIGURE 210

MAASLGQVLALVLVAALWGQTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFL
LNQCGSLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTWWRKTEAGVWD

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAACGGCTCTCTAGGCTCCAGCTTCCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCCAGCTGTCGAAAAGATTCCGCAATAAAACT
 TTGCCAGTGGGAAGTACCTAGTAGAAACGCCCTAAGATGCCACTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTGAGCTGTAGAATCTGTAGCTGCGTGAGTGTAAAT
 TCATGGAAAAATCCTGTGTCACAGCATTGCCCTGTAGATGCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTAGCCAGCTCTCTAGAGAACCCAGTCAGATTATACAGAACATATGT
 TCTGCTCAGCGGAGAACACTGCAGTGAGGAGAACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTCATTTGTAAAGCCAGTGCTGCCAAGGAAGGAATGCAGAACACCAG
 CGATGCCCTGGACCCCTCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGTTGTATG
 AATCTAATGGAACCTTCTGTGTGGAGCAGCTGGAAATGCTATGAAGAAGAACAGTGTGTCT
 TTTCTAGTTGAGAACACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGTGAAAGGCTGTTCT
 CAACGTCAGTAACGCCACCTGTCAGTCCGTCTGGTAAAACAAGACTCTGGAGGAGTC
 TCTTCGAAAGTTGAGTGTGCAAATGTAACAGCTTAACCCCCACGTCTGCACCAACCAACT
 TCCCACAACTGGGCTCCAAAGCTCCCTACCTTGGCCCTGCCAGCCTCTTCG
 GGGACTGCTGCCCTTGAGGTCCCTGGGCTGCACTTGTCCCCAGCACCCATTCTGCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCCTTTCCCTGCTCTGCCCTGTTAACTG
 CCAGTAAGTGGGAGTCACAGGTCTCAGGCAATGCCGACAGTGCCTTGTCTTCAATTATTA
 AACGACTGGTTCACTGCCAAAAAAAAAAAAAAAAAAAAAA

1252663

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCN SWEKSCVN SIASECPSHANTSCISSSASSSLET PVR
LYQNMFC SAENCSEETHITAFTVHVSAEEHFHFV SQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPWKC YEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFECANVNSLTPTSAPTTSHNVGSKASLYLLALASLLL RGLLP

FIGURE 213

GGCCTCGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCTCACTGGCCACCCCTCCAAACCCAAGAGCCCAGCCCC**ATG**GTCCCCGCCGCG
 GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGCGGGGGGCCAAGGCCTG
 ACCCAGACTCGACCAGAAATGCAGCGGGTCAGTTACGCTTGGGGGCCCATGACCCGCAG
 CTACCGAGCACGCCCGACTGGCTTCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACGCCCTGGCTGGACCAGCGGCTGCCGAGCTCTGGCCGCC
 ACGGTGTCACCGGTTAGCCGGTCGTCGCCATTAAACGAGGAGGTGGTCTTCAGAAGA
 GGGGTTGTGATTAATGCCGAAAGGATAGCACCAAGCAGAGAGCTCCAGTGCAGCTCCCA
 ATACAGCGGGAGTTCCAGCACGAGGTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAGCCTGCCCGCCTCCCCGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCGTCACCCCTACCCACAG
 CCATGCCATCTCTGAGGATCTGCGCTGGTGCTGATGCCCTGGGGCCGTGGCACTGCCAC
 TGCAAGTCGGGACCATGAGCGGAGCCGGCTGGGAAGCTGCACGGCTTCGGCGCC
 TCGAGTTGGGCGCTGAGCCAGCTCCGACGGAGCACAAGCCTTGCACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCTGGACACAAGTCTGTACTGACACCAACTG
 GCCTCTCAGAGCACCAAGTACCAAGGACCACCAACTACCCCTTCCCCACATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCCTGCCAGGCCCTGGCTTTGGAAACGGGTCA
 GGATTGCCCTGGAGGGATATTTGAATAGCCTCTTCAGTGTACAGAGATGCAACCAATA
 GACAGAAACCAAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTCAATCTAGCACCACTAGATATTTAGTACAGAAAAACAAACTGGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSÝRSTARTGLPRKTRI
ILEDENAMADADRLAGPAAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMPWGPHCHCKSGTMSRSRGKLGHSGRRLRVGALSQLTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTPFPTIHLRSSPSLPPASPCPALA
FWKVRIGLEIDIWNSLSSVFTEMQPIDRNQR

FIGURE 215

FIGURE 216

MAGLAARLVLLAGAAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWTVGGLYQEGHKVPQFHGKWPFSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPAASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLMLTVHSVSYLSLIRFDYGYNLVANVAIGLVNVWWIAWCLWNQR
RLPHVRKVVVVVLLQQLSLLDEPPPLFWVLDAAHAIWHISTIPVHVLFSSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

FIGURE 218

MAFQSLPSSRMAPLGMILLMMAACTFTCLSHQNLKEFALTNPPEKSSTKETERKETKAEEEL
DAEVLEVVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYYYHQMDNAQDLLSFGGLQVINGLNSTEPLVKEYAAF
VLGAAFSNPKVQVEAIEGGALQKLILVILATEQLTAKKKVLFALCSLLRHFPYAQRQFLKL
GGLQVLRTLTVQEKGTEVLAVRVVTLLYDLVTEKMFAEEEELTQEMSPEKLQQYRQVHLLPG
LWEQGWCEITAHLALPEHDAREKVLTQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
LELDQDGEDEGYFQELLGSVNSSLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGTTTCGGTTCCCCCCTCCC
 CTCCTCCGGGTCTGGGGTGACATTGCACCGGCCCTCGTGGGTCGCCTGCCACCCCA
 CGCGGACTCCCCAGCTGGCGGCCCTCCCATTTGGCTGTCTGGTCAGGGCCCCCACCCCC
 TTCCCACTGACCAGCC**ATG**GGGCTGGGTGTTTCGGCTGCACCTTCGTCGGTCCGGC
 CCGGCTTCGCTTTCTTGATCACTGTGGCTGGGACCGCTCGCGTTATCATCTGGT
 CGCAGGGCATTTCTGGCTGGTCTCCCTGCTGGCTCTGTGGTCTGGTTATCTGGT
 TCCATGTGACCGACCGTCAGCTGGGGCTGGGACCTACGGCTCTGATTTGGTGTGCT
 GTCTGCTCTTACAGGAGGTGTCGCTTGCCTACTAACAGCTGCTTAAGAGGCAGA
 TGAAGGGTAGCATCGTGAAGTGAGGACGGAAGATCACCCATCTCCATCGGCCAGTGGCCT
 ATGTTCTGGTCTCTCCGGTATCATCAGTGGTGTCTCTGTATCAATTTGGT
 GATGCCAGCTGGGGCCAGGTGTTGGGATCATGGAGACTCACCCATTACTTCGACTTC
 AGCCTTCTGACAGCAGCATTATCCTGCTCCATACCTTTGGGAGTTGTGTTTGTGATC
 CCTGTGAGAGGAGACGGTACTGGGCTTGGGCTGGTGGTGGAGTCACCTACTGACATCG
 GGACTGCACTTCTGGGACCCCTGGTATGGGCCAGCTGCTGCCATCTGCACTGT
 TTCCATGGGCTGGGCCCTCATCACAGCTGGGGGCTCCCGAAGTATTCAGGCAGCC
 TCTGTGTAAGGAG**TGA**CTACCTGGACTGATCGCTGACAGATCCACCTGCTGTCCACTG
 CCCATGACTGAGCCCAGCCCCAGCCGGTCTGGCCACATTCTCTCTCTGCTGCTGCTG
 GGTCTACCCACTACCTCCAGGGTTTGCTCTTGTGACCTTGTGACCTGTTGCTAAGCTT
 TACCAAGGAGCAGCTGGGTCAGCCAGTCACTGACTGGTGGTTGAACTGCACTTAC
 CACCACTGGGACCCCTGTGTCAGCAGGACTCCCCCTGTGTCAGTGTCTGCTCTCAC
 CCTGCCAAGACTCACCTCCCTCCCTGCAAGGCCAGGGAGACTGGGACACTGGGTGAT
 GGTGATATCTGCCCCTGGCATTCCCAGGAGACTGGGAGACCTAGGGGGACCCCTGGG
 CTGGGGTGCCTCTGTGATGTCCTGCCCTGTATTCTCATCTCAGTTCTGGAGCTGAG
 GTTGCCAAGAAAAGGGACCTAGTTAGCCATTGCCCTGGAGATGAAATTATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTCTCACTACTCCCTCAAGACTGGACATCTGGTCTTTCTC
 AGGCTGAGGGGGAACCATTTTGGTGATAAATACCCCTAACCTGCTTTTCTTCT
 GAGGTGGGGGGAGGGAGGGAGGTATATTGGAACTCTCTAACCTCTGGCTATATTCTC
 TCCTCGAGTTGCTCTCATGGCTGGCTCATTTCGGTCCCTTCTCCTGGTCCAGACCTT
 GGGGAAAGGAAGGAAGTGCATGTTGGAAACTGCCATTACTGGAACATAATGGTTAACCT
 CCTTAACCCACCACTCCCTCTCCCAAGGTGAGTGAGTGGAGGGTGTGTTGAGCTGGC
 CACTCCAGAGCTGCAGTGCACTGGAGGACTCAGACTACCATGACATCGTAGGGAAAGGG
 GAGATTTTGTAGTTAATTGGGTGTTGGGGGGGGGGGGAGGTTTCTATAACTGT
 ATCATTTCTGCTGAGGGTGGAGTGTCCCATCTTTAATCAAGGTGATGTTGATTGACT
 AATAAAAAAGAATTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

MGAAVFFGCTFVAFGPAPALFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIIFGAAVSVLLQEVRFAYYKLLKADEGLASLSEDGRSPISIRQMAVSGLS
FGITSGVFSVINILADALGPGVVGIGHGDSPYYFLTS AFLTAIILLHTFWGVVFDACERRR
YWALGLVVGVSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

FIGURE 221

AAGCTGGTTAACCGAACAGGAGGGTAGATTCGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTCTGGTCTCCCTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTGGCTGATGCANTTGGCCAGGTGTGGTGGATCCATGGAGAC
TCACCCATTANTTCCTGANNTCAAGCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCCTTCAGATGCCCGGTTCCACTACGGCTTCCCTGATTTTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTCCATCGCCAGATGGCCTATGTTN
TGGTNNTTCCTTCGGTATCATCAGTGGTGTNTCTGTTATCAATAATTGGNTGATGCAN
TTGGGCCAGGTGTGGTGGGATCCATGGAGANTCACCTATTAAATTCTGAATTAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTGGGAGTTGTGTTTTGATGCCTGTGA
GAGGAG

0909252111

FIGURE 223

NGTTGGAGAAGTGGCGGGACNTCATTGGGTTTCGGTTCCCCCTTCCCTTCCCCG
GGGCTGGGTGACATTGCACGGGCCCTCGTGGGTGCGTTGCCACCCACCGGGACTCC
CCAGNTGGNGGCCCTCCATTGCTGCTGGTCAGGCCAACCCCCCTCCACNTG
ACCAGCCATGGGGCTCGGGTGTTCGGCTGCACCTTCGTCGCGTTCGGCCGGCTTCG
CGCTTTCTTGATCACTGTGGCTGGGACCCGCTTCGGTTATCATCCTGGTCGAGGGCA
TTTTCTGGCTGGTCTCCCTGCTCCTGGCTCTGGTCTGGTCATCTGGTCCATGTGAC
CGACCGGTCAAGATGCCGGCTCCAGTACGGCCTCTGATTTGGTGCCTGCTCTGTCC
TTCTACAGGAGGTGTCGCTTGCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCTATGTTCTGG
TCTCTCCTCGGTATCATCAGGGTGTCTCTGTTATCAATTTGGCTGATGCACTTG
GCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTCCCNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCCTCGTGGGTCGCCTGGCACCCACGGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCTGCTGGTCAGGCCACCCCTTCCCACCTGA
CCAGCCATGGGGCTGCGGTGTTTCGGGCTGCACTTCGTCGCGTTGGGCCGGCTTC
GCGCTTTCTTGATCACTGTGGCTGGGACCCGCTTCGCCTATCATCCTGGTCGCAGGGC
ATTTTCTGGCTGGTCTCCCTGCTCTGGCCTCTGTTCTGGTCATCTGGTCCATGTGA
CCGACGGGTAGATGCCGGCTCCAGTACGCCCTCTGATTTGGTGTGCTGTCTGT
CTTCTACAGGAGGTGTTCCGCTTGCTACTACAAGCTGTTAAGAAGGCAGATGAGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCGCCAGATGGCTATGTTCTG
GTCTCTCCCTCGGTATCATCAGTGGTGTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGATCCATGGAGAC

FIGURE 225

CCCCCAGGGAGCACGTGGTGGTTATAACTCAGGCCGGTGCCAGAGGCCAGGAGGAGGCAG
TGGCCAGGAAGGCACAGGCTGAGAAGTCGCGCTGAGCTGGGAGCAAATCCCCACCCCC
TACCTGGGGACAGGGCAAGTGAGACCTGGTGGGGCTCAGCAGGCAGGGAAAGGAGAGG
TGCTGTGCCCTGCCACCATCTTCTCTGTCCCCTGCCGTGCTGGAGGCTGCT
AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGCTCAGCGCAGTGCATGGTGGCCCGT
CCTTGATGTGGGTGCTCTGCTGATCACAGCCTTGCTCTGGGGTACAGACATGTT
CTCGCCAACAATGATGTTCTCTGACCACCCCTAACACCCCTGCCCTGGGAGCAACCA
GGACCTGGGAGCTGGGCCGGGAAGACGCCGGTGGATGACAGCAGCAGCCGCATCATCA
ATGGATCCGACTGCATATGCACACCCAGCGTGGCAGGCCGCGTGGCTAAGGCCAAC
CAGCTCTACTGCGGGCGGTGGTGTGATCCACAGTGGCTGCTACGGCCGCCACTGCA
GAAGAAAAGTTTCAGAGTCCGTCGGGCACTACTCCCTGTCACCAAGTTATGAATCTGGG
AGCAGATGTTCCAGGGGGTCAAACTCATCCCCCACCTGGCTACTCCACCTGGCACTCT
AACGACCTCATGCTCATCAAACGAGAATTCGTCACAAAGATGTCAGACCCAT
CAACGTCCTCTCATGTCCTCTGTCGGGACAAAGTGCTGGTGTGCTGGCTGGGACAA
CCAAGAGCCCCAAGTGCACTTCCATAAGGCTCCAGTGCCTGAATATCAGCGTGTAAAGT
CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCCGGTGA
CAAAGCAGGTAGAGACTCTGCCAGGGTGATTCTGGGGGCTGTTCTGCAATGGCTCC
TGCAGGGACTCTGTCCTGGGGAGATTACCCCTGTCGGGGCCAAACAGACGGGTGCTAC
ACGAACCTCTGCAAGTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC**TGA**GTCA
CCCAGGACTCAGCACACCCGATCCCCACCTGCTGCAGGGACAGCCCTGACACTCTTCCAG
ACCCCTCATCTCCAGAGATGTTGAGATGTTCAATCTCCAGGCCCTGACCCCATGTC
CCTGGACTCAGGGCTGCTGCTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCTGG
GAACAAATTCCAAAAGTCTCCAGGGCGGGGGTGCCTCAATCTCCCTGGGGACTTCT
CCTCAAGCTCAGGGCCCATCCCTCTGTCAGCTGACCAAATTAGTCCAGAAATAAA
CTGAGAAGTGGAAAAAA

FIGURE 226

MATARPPWMWVLCALITALLGVTEHVLANNDVSCDHPSNTVPGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLTAHCRKKVFRVRLGHYSLSPVYESGQQMFQGVKSIPHGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCP SAGTKCLVSGWTTKSPQVHF PKVLQCLNISVLSQKRCEDAYPRQIDDTMFCA GDKAGR DSCQGDGGPVVCNGSLQGLVSWGDYP CARPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGCGGCGCTGCCAACTGAGGACC^GCCGCGCAGA
 CAAGCCGCA^GGGGCCAGCTGCGGCTACGTGCTGTGACCGTGCCTGGCCCTGGCTGTGC
 TGGTGGCTGTAGCTGCA^CCCGGTGGCGCTCTTCCTGAACCACGCCACCGC^GGGGCACG
 GCGCCCCCACCTGCTGCTGACTGGGCTGCCAGCGAACAGCGCCCTGGTCACTGTGGA
 AAAGGGCGGACAGCTCGCACCTCAGCATCCTCATGGAGACCCGCGCTGCCCGAACCTCACCAGA
 GCTTCGCA^CGCTGGAGAGCGCCCAGGCTCGTGTGCTGAGGCGCTGACAGAGCACCAAGGCC
 CAGGCCACGGCTGGTGGCGACCAGGACGAGGACTGTGACACGCTGGCCGACCCAGCTGCC
 CCGGCTGCTGGCCCGAGGCTCAAGCTGCTGAGGCGATGCTGGAGACATGGGCTGCGGAAGGGCATG
 GCACGGTGGGCCAGGGCTCAGGCCCTGCAGAGT^GAGCAGGGCCGCTCATCAGCTTCTC
 TCTGAGAGGCCAGGGCACATGGCTACCTGGTGAACCTCGTCA^GGACATCCTGGATGCCCT
 GCAAGAGGACCGGGGGCTGGCCGGGGCGAACAGCGGCCACCTT^CAGAGAGGCCCTGCC
 GGGAAACGGCCCGGGGGCTGTGCACTGGTCTCCGGCCCGAGACTGTGAGCTCTGCC
 CTAAGCGACAGCAGGAGCATGGCTACTCTGTCTTTCCCACCAACTACCGCCGGGCTT
 CCAGGTGACTGTGACATGGCACGGACGGCCGGCTGGACGGTGTGTTTGCGGCCGGGAGG
 ACGGCTCCTGTA^ACTTCTGGGGCTGGGAGCTTACCCAGAGCGGTTTGGCAGGCTCACC
 GGGGAGACTGGCTAGGGCTCAAGAGGAT^CACGCCCTGACCACAGGCTGCC^TACGAGCT
 GCACGTGACCTGGAGGACTTGTGAA^TGTGACGCCCTATGCCGCTACGGGAGCTTGGCG
 TGGGCTTGTCTCTGGGACCCCTGAGGAAGACGGGTCA^CCTGGTCACTGGTGTGATTCTC
 GGCAC^TGTGAGGCGACTCCCTGTA^CACAGCAGGCCATGAGGT^TCA^CCCACCAAGGCCGTGA
 CAGGACACATTAGAGAACACTGTGCCCTTCA^TACCGCCGGTGCCTGTGGTACCGAAC
 GCCACACGCTCAACCTCATGGCA^CACTTACCTGGCCGGTGC^CCC^TCTGTGGCAGGCC
 GTGGAGTGGCTCTGGACCCGCTGGAGCTACTAC^TACTCA^TCTGTGAGATGA^AGTCCG
 GCGGCTCGGGAGGACCC^T**TAG**ACTGGTGCACCTTGTCTTGGCC^TTGTGGTCTCTGTGC
 CCCATCCCAGGCCACCCACTCTCTGGTGAAT^TTCTCACCACCTGGCTGGCG
 CCAC^TCTCCAGTAGGGAGGGCCGGG^CATCTCGACAGAAGCTTGGCC^TTGTGATTCTGGCT
 CACACATCGCCCTCTCGCCGCTCCACCCACCCCTCCATTGGCAGGTCA^TCTGTGACTCTGGCT
 TGCTGATGGGGCTGGCAA^TCTTGACGACCCCAACTCTGGCCTGTGCCCCACTGTGACTCCGG
 TGCTGTTGGCTTCCCCTGGCAGGATGGTGGACTGTGCCCCAGGCCCTCTGGCTGGCC
 GGCAAATAACCGGCAATTATGGGAGACAGAGCAGGGGAGACAGCACCCCCCTGGAGTCTC
 CTAGCAGATCTGGGGAA^TTGTAGGTCTCTGAGGT^CAGGTCTGAGGCTCAGGCTGAGGCTATCTCCAG
 CCCATCCCAGGCCACCCACCCACCCCTGGCTGGCCAGGAACCCACCTCTCCCCAA
 GGGCCTCAGGCTGGCTGGCTGGGCTGGCCCATCTTAC^CAGGAGGCC^TGAGGT^CAGGATGGG
 GAGGCTGCTGCCCTTGGGACCCACGCTCCAAAGGCTGAGGAGGACTTCCCTGGGAGGCCAC
 CCTGTGCCCGGAGGGCTGGGCTGCTGAGGTCTCTTACCTGTGCCCCACTGTCTCTG
 TCTCAAATGAGGCCAACCCACCCACCCAGCTCCGGCCGCTCTTACCTGGGGCAGC
 CGGGCTGCCATCCATTCTCTGGCTCTGGAA^TGTTGGGCTGGGCTAGGAGGGCTGGGATGAG
 GGACTGGCTAATGGGAA^TCTTGTGTTCTGGCTGGGCTAGGAGGGCTGGGATGAG
 GCTTGTACAACCCCCACCCACCAATTTC^CAGGGACTCCAGGGTCTGGCTGGGCTCCAGGAGG
 GCCTTGGGGGTGATGACCCCTTCCCTGGGT^CAGGTGCTCTCATGAGGAGGCCAACCTTGCC
 ATTGACCC^TGGCCACCTGGACCCAGGCCAGGGCCGGGGGGGGGGGGGGGGGGGGGGGGGG
 CCACCTCACCGGGCAATAGGGTGTGGGGGACTGGGACCCAGGACAGGCCAACCTGGACA
 CTTTCTGTGTA^ATCTCCCAACCCAGCAGCTGTCA^TCCACTCTTGTGACACAA
 TGCAGAGGT^GAGACCCCGAGGCTCCAGGACAGCAGGCCAACGGCAGGGCTGGACCCGG
 TCCTCAGGTGTCTGCTCAGGCCCTGGACCCGCGTGC^GGT^TACCTCAGGCCAGATGCA^GGG
 CGGCTTCTCCAAGGGCTCTCTGATGGGGGCTCCGA^AAGGGCTGGAGTCAGCCTTGGGGAGCT
 GCCTAGCAGCCTCTCTGGGAGGGAGGTGGCTTCTCTCAAAGGACACCGATGGCA
 GGTGCTCTAGGGGTGTGGGTTCCGTTCTCCCTCCACTGAAGTTGTGCTAAAA
 AACATAATAATTGACTGGCACCACTGGGGTTGTGGAGAGGCCGTGACCTGGCTCTC
 TGTCCCAAGTGGCACCAAGGT^CATCCACATGCGCAG

FIGURE 228

MVNDRWKTMGAAQLEDRPRDKPQRSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQ^A
QPRLVGDQEQUELLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQGR^BL^CIQLL
SESEQGHMAHLVNSVS^DILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDV^EL
LSGQQDDGVYSVFP^FHYPAGFQVYCDMRTDGGGWIVFQRREDGSVNFFRGWDAYRDGFGR^GLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENG^HTAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKHSGMRFTTKDRSDHSENNCAFYRGAWWYRNCHTSNLNGQYLRGAHASYADG
VEWSSWTGWQYSLK^IKFSEM^JKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTAGTGCCT
 TGCTTCTGAACTAGCTCACAGTAGCCGGCGGCCAGGGCAATCCGACCACATTCACTCT
 CACCGCTGTAGGAATCCAGAT**TG**CAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGACACCAACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTGGCATTCCAGAGCCC
 CGGCGCACAGAGCACAGGCTCCCTCAAGCTGGCAGCCAGTGGCCTGACCCCTGCTGAC
 TTTGTGCTTGGTGTGCTGATAGGGCTGGCAGGCCAGTGGGCTTTGTTTCACTACTACCC
 AGCTCTCCAATACTGGTCAAGACACCAATTCTCAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTGTCAATCTCTCAAGTCCAGAAATATAAAGCTTGCGAGGAAGTCTGCAGCATGTGGC
 TGAAAACACTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTGTACAG
 AACAAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAGTGGGAG
 GACTGTAAATATTCTGCCTTAGTGAAGAACTCTACCATGCTGAAGATAAAACAACAAGAAGA
 CCTGGAAATTGCGCGTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGGCTT
 TGCGCCCTGACAGTGGCAAGGCCCTGGCTGGATGGATGGAACCCCTTCACCTCTGAACCT
 TTCCATATTATAATAGATGTCACCAGCCAAGAACAGAGACTGTGTGGCATCCTCAATGG
 GATGATCTCTCAAAGGACTGCAAAGAATTGAAGCCTGTGTCTGTGAGAGAACGGGAGGAA
 TGGTGAAGCCAGAGGCCCTCATGCCCCCTGAAACATTAGGCAAGGTGACT**TG**ATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCCGTGCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAATGGGTTCTCGT
 TTTCTTCTCAGGATCACCAGCATTCTGAGCTGGTTATGCACGTATTAACGTACA
 AGAAGTCTTATTACATGCCACCAACCAACCTCAGAACCCATAATGTCATCTGCCCTTCTG
 GCTTAGAGATAACTTTAGCTCTTCTCTCAATGCTAAATATCACCTCTGTTTCT
 GTCTCTTACACTGGTGGAAATAAGAAACTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCTCTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACCTCCAGATTGTAC
 AGCAAATACACAAGGAATTCTTTGTTGTTCTGAGTCAACTAGTCCCTCCAATCCAT
 CAGTAAAGACCCCATCTGCCCTGTCCATGCCGTTCCAAACAGGGATGTCAGTGTATGAG
 AATCTCAAATCTCAATGCCCTATAAGCATTCTCTGTGTCTTAAAGACTCTGATAATTG
 TCTCCCCCTCATAGGAATTCTCCAGGAAAGAAATATATCCCCATCTCCGTTCTATCAG
 AACTACCGTCCCCGATATTCCCTCAGAGAGATAAAGACCAGAAAAAGTGAACCTTCA
 TCTGCACCTGTAATAGTTCTGAGTCTATTCTCCATTGACCCATATTACCTTCA
 GTACTGAAGATTTAATAATAAAATGTAATACTGTGAAAAA

230/330

FIGURE 230

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRTTEHRAPSSTWRPV
VALTLITLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWECKYFCLSENSTMKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

FIGURE 230

FIGURE 231

AATTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTGCCACAATTCCGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTCCTGGTCTGCTGATAAGGGCTGGCAGCCCTGGGCTTTGTTTTCAAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAATGAAAGAAAGATTAGGAAATA
CGTCCCAGAGTTGCAATTNTCAAGTCCAGAATATAAAGCTTGAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTGAAAGGAGGGCAA
AGTNCTCATNTACTATACACACACCCACTTCCC

FIGURE 232

GCGGAGCCAAAGAACCTGCGCAGCCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCAGCGCTC
 CGGGGATTGCGCTCGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGGCAGGGCCCGCCGCCGGGG
 CCCGAGCCCTCCGGATCCGGCCCCCTCCCGGTCCGGGCCCCCTCGAGACTCCTCTGGCTGCT
 CTGGGGGTTCGCGGGGGCGGGGGACCCCGGGTCCGGGCGCATCGCTGCTGCTGCTG
 TCGGTCTGCGGCCCGCAGGGCCGTGGCGTGGGCATCTCCCTGGGCTTCACCCTGAGCCT
 GCTCAAGCGTCACTTGGGTGGAGGAGCGGTGCGGCCAGGGCCGCCAACCTTGAGACTCTG
 AGCTGCCGCCGCGGCAACACCAACCGGGCGCCGGCCAACCTCGGTGCGAGGGAGCG
 GAGCGCAGAAGCCCAGGGCGGGCGAAGGCGCCGGAGAATTGGGAGCAGCGCTTGGC
 CTACACACCTGCGACAGCCGGCAGGGCCCAAAGGCGCTGAGGACCGCTACATCAGCA
 CGGAGCTGGGCATCAGGGCAGGGCTGCTGGCTGGGCTGACTCTCAGACACAGCTGCC
 ACGCTGGCGTGGCGTGAACCGCACCTGGGGCACCGGTGAGCGTGTGGTCTTCATGAC
 GGGCGCACGGGGCGCCGGGCCAACCTGGCAGTGGCAGTGGTGACGCTGGCGAGGAGCAG
 CCATTGACACCTGACCTGGCGTGGCCACCTGCTGGACAGCACGGCAGACTTTGAC
 TGGTTCTCTGGCTGCTGACACCACCTAACCGAGGGCAGGCCCTGGCAGCTTAACCTGG
 CCACCTCAGCGTGGCCCGCCACCTGTAACCTGGGCCGCCCCAGACTTCATGGCG
 GAGAGCCCCACCCGGCGCTACTGCCACGGAGGCTTGGGGTGTGCTGCGCGATGCTG
 CTGCAAAACTGCGCCCCCACCGGTGGAAAGCTGCCAACAGACATCGTCACTGGCCCTGA
 CGAGTGGCTGGGCTGCTGATTCTCGATGCCACGGGGTGTGGCTGACTGTGACCAAGGAG
 GGGTGCATA TAGGCATCTGGAGCTGAGCCCTGGGAGGCACTGGCAGGAGGGGACCCAT
 TTGCGAAGTGGCTGAGCAGGCCACCTGTGCTGACCCCTGGCAGCTACAGCTGACCAA
 AGCTTCCGGCCAGCTGAACTGGAACGACGCTGACCCAGGAGATCCAGGACTACAGTGGAGA
 TCCAGAATACCAAGCCATCTGGCGTTGATGGGGACGGGGCAGCTGCTTGGCCCTGGTATT
 CCAGCACCATGGCCGGCCCTCCGGCTTGGGACTCTGGCTGCTGGGACTACTTCACGGAGCA
 GCACGCTTCTCTGGCCGGCCCTGGCTGCTGACCCCTGGCAGCTGGGGCTGACCGGGCTG
 ATGTTGGCGATGTTCTGGGAGCAGCTGAGGAGCTGACCCCTGGGAGGCACTGGCAGC
 CCGCTCAGAACAGCAGCTGTGATGGCTACGGCCTGGGAGGCTGGGAGGAGGGGGTATGGA
 ATACACCTGGACTTCAGCTGGAGGACTGACCCCTGGGAGGCCGGCCCTCACTC
 GCCGAGTCAGCTGCTGGCCGGCTGAGCGCGTGGAGATCTGGCTGTGCCCTATGCTACT
 GAGGCTCACGCTCTCATGTCGCTGCTCATGGCTGGCCCTGAGCGTGAACCTGGCCCTGG
 CTTCTGGAGGCTTGGCACTGCACTGGAGGCTGGTGTGATGCTGCGGAGGCCATGACCC
 TGCTGCTACTGATGAGCCGGCCAGGGCCAGGGCTGGCCATGAGATGTCCTGGCACCT
 GTCAAGGGCCACCTGGCAGAGCTGAGCGCTTGGGGTGGGGGGTGCATGGCTCAG
 TGTGAGACAGCCGACCCCTACCAACTGGCCTCATGGATCTACTCTCCAAAGACGCC
 TGGACACACTGTTCTGCTGGCCGGCCAGACGGCTGAGGAGATCTGGCTGTGCCCTATGCTACT
 TGCCGCTGATGCGCATCTGGCCGGCTGGCAGGGCTTGGCTTCCATGCACTTCCAGCCTTCCA
 CCCAGGTGTGGCCCCACCAAGGGCTGGGGCCAGAGCTGGGGCTGACACTGGGGCT
 TTGATGCGCAGGAGCCAGGGCTGGGGCTGGCTTCAACTCCGACTACGGCAGGCCCTGG
 CGGCTGGCGCAGGCTCAAGAACAGAACAGGAGCTGCTGGAGAGGCTGGATGTA
 GACTGTTCTCCAGTCAGTGTGCTGGGGCTGGAGGGGGCTGAGCTGGGGCT
 ACCGGGCCCCAGACGCTGCGAGGGCTGAGGCTGAGGAGCTGGAGGGGGCTGAGGCT
 GTGCTTGAGGGCCTGGCTCCCGAACCCAGCTGGCATGCTACTCTTGAA
 CAACAGCACCTGAGCCCCACCCACTGCTGGGGCTGGGGCTGGCAGTGGCAGC
 ACAGGAGGGGGCTGGGGCTGGGGCTGAGGAGCTGGGGCTGACCTGGGGCT
 CTCCCCAAAACAGAGGCCACCTGGCAGGCCCTGGCTGGGGCTGGGGCTGAGGAG
 AACGTTGGGACTGGTCCCTCTGGCTGTGGGTCCCTGGCTCTGGACAGGACTGG
 GGACGTTGGGCCCCAGAGCCAGGGGGCTGGGGCTGGAGGGGGAGCTGGGGCT
 GCTGATTCGGGCTGGGCTCCACGTATTATGCACTGAGTCTGCTGACCCAGGCC
 CTCTGGGGCTGGGGCTGGGCTGAGAAGAGTTGGGGAGGGAGCTGAGGAGGG
 GCATCTCCAACTTCTCCCTTTGGACCCCTGGCGAAGCTCCCTGCTTTAATA
 AACCTGGCCAAGTGGAAAAAA

FIGURE 233

MRA SLLL SVLR PAGPV AVG I SLGFT LLS VTW VEE PCGP GPP QPGD SEL PPR GNT NAA RRP
NSVQ PG AERE KPGAGE GAGEN WEP RVLPY HPA QPGQA AKKAVRTRY I STELGIR QRLL VAVL
TSQT TLPT LGVAVN RTL GHRL ERV VFLTG ARGR RA PGM AVVT LGEERPI GH LHL ALR HLL E
QHG DDF DWFFL VPDT T YTEAH GLAR LTGH LSL ASAAH LY LGP QDF FIGGE PT PGRY CHGG FG
VLLS RMLL LQQLR PHLEG CRNDIVS ARD EWL GRCI LDAT VGCT GDHEGVH YSH LEL SPGE P
VQE GDPH FRS ALTAH PVR DPV HMY QLHK AFARA ELERTY QEI QEL QWEI QNT SHL AVDG DRA
AAWP VG I PAPSRP ASR FEV LRWDY FTEQ HAFSC ADGS PRC PLRGAD RA DVAD VLGT AEEL N
RRYHP AL RLQK QQLVN GY RR FD PARGMEY TLDL QLE ALTP QG GRPL T RRV QLLR PLSR VEI
LPV PVY VTEAS RLT VLL PLAAA ERDLA PGF LEAFATA ALE PGD AAA ALT LLL YEP RQ AQR VA
HADVF APVK AHVA ELLERR FPGAR VPW LS VQ TAAPS PLR LMDL SS KKHP LDT LFLL AGPDT VL
TPD FLN RCRM HAIS GWQ AFF PMH FQAF HPGV APP QGPG PP E LGR DT GRF DRQ AASE AC FY NS
DYVA ARGL LAA ASE QEE ELLES LDV YEL FLHF SSI LV RAVE P ALL QRY RA QTCS ARL SEDL
YHR CLQS VLE GLGS RT QLAM LL FEQ EQGN ST

FIGURE 234

GCTCTGGCCGGCCCCGGCATTGGTCACCGCCCGTAGGGGACAGGCCCTGGCCTCCCTGTAT
 TGGCAAGCGCTGGCACCTCCCCACACCCCTTGCACAGCTCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTGGCAGGGCCCCTTTAGAAGCTTGATTCCTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCCTTTCCCTAGTGGCGAGGGAACTCGGGGCGATTGGCTGGAA
 CTGTATCACCCAAATGTCACCGATTCTCCATGCAGGAATGAGCAGACCCATCAATAA
 GAAATTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACGGAGCAAAG
 AGGGTTGCTCAACGCCCCGCTCATGGAAAACCAATCAGATCTGGGACCTATATAGCGT
 GCGGAGGGGGCGATGATTGTCGCCTCGCACCCACTGCAGCTGCGCACAGTCGCAATTCT
 TTCCCCGCCCCCTGAGACCCCTGCAGCACCATCTGTC**ATG**GCGGCTGGCTTTGGTTGAGC
 GCTCGCCGTCTTGGCGGAGCGGCAGCGAGGGCTCCGGCGCCGCGTCCGCTGG
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCGTCCCTGTGGCGGGAAAGCGGCCCAAGAAC
 CGACCAACCCGTGCAAGAGGACCCAGAACCCGAGGAGCAGAAAATTGATGAGAAGAACCC
 GACTCCCATGGTTATGACAAGGACCCGTTTGGACGTCTGGAACATGCGACTGTCTCTT
 CTTGGCGTCTCCATCCTGGCTTGGCAGCACCTTGTGGCTATCTGCCGTACTACA
 GGATGAAAGAGTGTTCCCGCCGAGCTGAGAGGCTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATGGAATCCAAGTCTGACCCAGAACATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAACGCCCTCCCCACCCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPS A VAGKRPPEPTTPWQEDPEPE
DENLYEKNPDSHGYDKDPVLDVNMR LVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 236

GGCGGCTGGGCTGTTGGTTGAGCGCTGCCGTCTTGGCGGAGCGGCACGCGAGGGC
TCCC GGCGCCCGCTCCGCTGGGAATCTAGCTTCAGGACTGTGGTCGCCCGTCCGCT
GTGGCGGGAAAGCGGCCCGAACCAGACCCGACCACACCGTGGCAAGAGGACCCAGAACCGAGGA
CGAAAACCTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGGACCCGTTTGGACG
TCTGGAACATGCGACTTGCTTCTTGGCGTCCATCATCTGGTCCTGGCAGCACC
TTTGTGGCTATCTGCTGACTACAGGATGAAAGAGTGGTCCCGCGCAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCTTCCATCATGGAATCCAAGTGCCTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCCTGCTCGCCCTGGCTCCTGGGGCCCGGGCTGGTGCCT
 TGCAAAACCCACCGCACAGCCTGGGGAGGAACCTGTATCACCCCGCTGCCCTCCGGG
 ACGTAGCCGCCACATTCCAGTTCGACGCCGCTGGGATTCCGGAGCTTCAGCGGGAAAGGAGTG
 TCCCATTAACAGGCTTCCCAAAGGCTGGGGCAGCTGATCTCAAGTATTCTACGGGA
 GCTGCACCTGTCATTACAACAGGCTTGGAGGACCGATACTGGGGCCACCCCTCTGC
 AGGCCCATCAGGTGAGACTGTGGTCTGGTTCAAGAACACTGTACTGATGTGATAAA
 TCTTGGAGGAGCTCAGTAATGTCCTCAGGGATCTTCTGGCCTCTCTCAACTCATCGA
 CTCCACCAACACAGTCACTCCACTGCCCTCTCAACCCCTGGCTCTGCCCAATGACACTG
 ACCACTACTTCTGCCGCTATGTCGCTGCCGGAGGTGGTCTGACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTGCCCTGAGTCCAAGGCAGGCCCTCTGTGCTGCTGAAGGAGA
 TCGCTTCCACACAGCTTACACTCCAGGCAGTCATACCGCCCTGTGAGTTGAGAAAATG
 CACGCTGACTAGCATCTCCGGAGCTGAGGCAAGGCCCTGTGAGTTGATGCCCTC
 ATCACGGGAGGAAAGAACACTGGTCCCTTCCGGATGTTCTCCGAACCCACGGGA
 GCCCTGCCCCCTGGCTCAGGAGCCAGTCTATGGAGACATCACCACCTAACACGGAGA
 ACGAGACATAGGGTGACCCGGACCAACTATCAGGACGTATCCTAGGGACT
 CGGAAGACCTATGCCATCTATGACTGTCAGACCCGCACTGATCAACAACCTCGAAACCT
 CAACATCAGCTCAAGTGGAAAGAGACCCCAGAGATGAGGCCCCCAGTGCCTCTCTGC
 ATGCCAGCGTAGTGGCTATGGCTGAGGAGCTGAGGACACTGCTGTTAC
 AACACCCACCCATACGGGCCCTCCGGCTGCTGCTGGACACCGTACCTGGTATCTGCG
 GCTGTATGTGACACCCCTACCATCACCTCCAAGGCAAGGAGAACAAACCAAGTACATCC
 ACTACCGCCCTGCCAGGACCGCTGCAAGCCACCTCTGGAGATGCTGATTCACTGG
 GCCAACCTAGTCACCAAGGTTTCCATCAGGTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCTAACCATGGCTCTATGTCAGCCCATCTGTCTCAGGCCCTTGGCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGACTCCCTCTCACAGCTGTTCCCA
 GTCTCTGATGGCTTAACACTTTGCGGCTCTACACGGAGCCGCTGCTGGGAACCTGCC
 GACACCCGACTTCAGCATGCCCTACACCGTATCTGCCCTACCTGGGACTCTGGTGGCCGTGT
 GCTACGGCTCTTCAACATCCTCACCGAACCTCCACATCAGGAGCCCCGACAGGT
 GGCCCTGCCAAGCCGCTGGCAACCTTATCGGCCGGCCGAGGTGCCCCCAGT**TGATT**
 CTTGCCCTTCCAGCAGCTGCGCTTCTCTGGGGAGGGAGCCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCTCAGAGTGGCTTTGAACCAAAGTGCCTGGACAGGTAGGGC
 CTACAGCTGTGTTGCTCAGGAGCACGAGGCAATGTGGCATTGAAATTGAATTA
 CTTAGAAATTCAATTCTCACCCTGAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAA
 AGTGGTGGCTGGCTGTTGATGGACAGCACAGAAAAGATTCCATCACACAGTGTATGTC
 ACTGTCAGTGTAGTGGAGGTC
 GGAGTTACTGTTGTGGAATAAAACGGCTGTTCCGTGGAAAAAAAAAAAAA

FIGURE 238

MPLALLVLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSRELHLSFTQGFWRTRYWGPFLQAPSGAELWVWFQDTVTDVDKSWK
ELSNVLSGIFCASLNFDSTNTVPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSISWELRQTLSVVFDAFITG
QGKKDWSLFRMFSRTLTECPCLASESRVYVDITTYQDNETLEVHPPPTTYQDVILGTRKT
YAIYDLDTAMINNSRNLNQLKWKRPENEAPPVFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTVPWYLRLYVHTLTITSKGKENKPSYIHYPQAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAKPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLPTPDFSMVNIVICLTCTVVAVCYGSFYNLLRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTGGTCCTCATGGTGTCTCTCGTTCTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTGCCAGCTGACAACGTACGC
TGCTTCAGTCAGTCCGATCTCCCCAGTGTACACAGACCAGGACTGTCAGGGAAAGGAAGTG
TTGTTACCTGCAGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGCAAGGCCATACCCCTGAGCAGGATGGAGGCAAGTGTCCAGGC
TCCTCCTTACCAAGGGTGCCTCAGAAATGATGCTGGGTCTTCTACCTCTGGGGTCACTC
TCACCTGGCACCTGCCCTGAGGGTCTGAGACTTGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTGAAGTCTTCCCCAAAAGAGGGAAAGAGTCACAAAAAG
TCCAGACCCCCAGGGACGGTACTTCCCTCTACCTGGTGTCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTATAAGAGACCCCCAAGAGCTGCCCTTGCCCTTC
TGCAATGTGATCACAGCTAGAAGGCAGTGTAGAGAAGAGAAACTGGTCTCACCAAGATG
CTGAATCTGCTGGTGCCTTGATCTGGACTTCCCAGCCTCTAGAACTGTAAGAAATAATAT
TTGCTGTTATAATCCAA

FIGURE 240

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQQDCLGERKCC
YLHCGFKCVIPVKELLEGGNKDEDVSRPYPEPGWEAKCPGSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACCTAGCACTTGCGGGAGTGGCTATTGTTAACAAAGGGTGTGCACCTCTGGCAGG
 AAACCTAGCGGTGAGACTCCAGCTGCCATCACAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCGACCCACC**ATG**AGGTCCTGCCCTGGAGATGCAGGACCTGAGCCAAGG
 CGTCCAGTGGCTTCTGGCTCTGGCTCTGGCTCTTCCTTCGCCCCCTTTTA
 TTAAGGAGCCTCAAAACAAAGCCTTCAGGCATCAACGACAGAGAACATTAAGAAGGCT
 CTACAGTCCCTGGCAAAGCCTAACAGTCCCAGGCACCCACAAGGGCAGGGACAAACATCTA
 TGCAGACCAGCGCCAGAGAACATGCCTAACACACACAAACCCAGGCCAAGGCCACACCA
 CCGGAGACAGAGGAAGGAGGCCAACAGGCACCCGGAGGACAGGACAGAACAGTGGCCAC
 ACAGCACAGGGCAGCATGGAAAGAGGCCAACAAAAGAGAACATGGTAAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGCCCTCTGGCAGGACAGGACAAATCATGGAAGAGCC
 AGGACACAAAGACGCCAACGAAATGGGGCCAGACCCAGGAAGCTGACGGCTCCAGGACG
 GTGTAGAGAAGCACGGGCAAGGCCAACACACAGGCCAACAGGCTCATTCACAAAGTC
 GCACAGAAATGCTGCCCTCACAGGAGCAGTGTCAAAGGAGCAGAACAGGAGTGA
 CAGCAGTCATCCACCTAACAGGAGAACAAACCTCAAGGCCACCCACCCCCCTGCCCTTCCAG
 AGGCCACAGCAGCAGAACAAAAGACTGAAGGGCCGCAACTTCAAATCTGAGCCTGGTG
 GGATTTGGAGAAAAAAATACAGCTCGAAATAGGAGCCTTCAGCAGACTGCCCTGACTCTG
 TGAAGATCAAAGCCTCAAAGTCGCTGTGGCTCCAGAAACTCTTCTGCCAACCTCACTCTC
 TTCTGACTCCAGCACACTAACAGAGTGAAGGGACGCCCTGGGAACACTTGTGACCA
 CTTGGCCTCATGGAGCTCAACTACTCTTGGTGCAGAGGTCCTGACACGCTTCCCTCAG
 TGCCCCAGCAGCTGCTCTGGCAGCCTCCCCCTGGGAGCCTCGGTGATCACCTGT
 GCCGTGGGGCAAGGGGAGCTCTGAACAACTCCACATGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCAGTGGAGCTCTCAATTAAAGGCTACGAACAGGATGGGGACTC
 GGACATCTCTACAGGCTTACGGCCTCTCCCTGAGCCAGTCAGTCACTCTTATATTGGCAAT
 CGGGGTTCAAGAACGTGCCCTTGGGAAGGACGTCGCTACTTGCACTCTGGAAAGGCAC
 CGGGGACTATGAGTGGTGAAGAACACTCTTATGAATCAGACGGTGTAGTCAA
 AAAACCTT
 TCTGGTTCAGGCAAGACCCAGGAAGGCTTCTGGGAAGGCTTCAGACATGGACAGGTA
 CTG
 TTGCTGACCCAGACTTCTCGATACATGAAGAACAGGTTCTGAGGTCTAACGCCCTGG
 TGTTGGGCAACTGGAGATACGGCCCAACACTGGGCTCTGCTGACTGCCCTTC
 AGCTCTGACCAAGGTGACTCTTGGCTCATCACTGAGGGCCATGAGGCCCTTCTGAT
 CACTACTATGATACATGGAAAGGGCTGATCTTACATAAACCATGACTTCAAGTGG
 GAGAGAACTGAGTGGCAAGGGCTACAGATGAAGGGATAATCGGCTGTACAGCTGCTGG
 CGGGAACTGCAAAGCCAAGAC**TG**ACGGGCGCAGGGCTGCCATGGTCTCTGGCTC
 CAAGGCACAGGACTGGAAACTTCTGAGACTCTTGGCCATTCCCATGGCTCAGACTAA
 GCTCAAGGCCCTCAGGAGTTCACAGGAAACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAATTGAGGTTCTGAAGTCTTCAGTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTTAATTAAATGGGGTGTGGGTGGCCAATACCCACAAATTCTGCTGAAA
 AACACTCTT
 CCAGTCCAAAGCTCTTGATACAGGAAAGAGCCCTGGATTACAGAAACATATAGATCTG
 GTTGAAATTCCAGATCAGGTTACAGTTGTGAAATCTGAGGTATTACTTAACTTCACTAC
 AGATTGCTAGAAGACCTTCTAGGAGTTATCTGATTCTAGAAGGGCTATACCTGCTT
 TCTTTAAGCTATTGACAACCTACGTTGTTGAGAAAAGTGTAAATACAAATGATGTT
 GTCCATGGAAAGGCAAATAATTCTACAGTGAaaaaaaaaaaaaaa

FIGURE 242

MRSCLWRCCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTQPSRQHRTENIKERSLQLSLAKP
KSQAPTRARRTTIYAEPAPENNANLNTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
KSPEKEKTMVNTLSPRGDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTAASRTVSEKHQG
KAATTAKTLPKSQHRLMLAPTGA VSTRTRQKGVTAVIPPKKEKKPQATPPPAPFQSPTTQRN
QRLKAANFKSEPRWDFFEEKSFEIGLQTTCPDSVKIKASKSLWLQKLFLPNLTIFLDSRH
NQSEWDRLEHFAPPFGFMELNYSLVQKVVTRFPVVPPQQQLLLASLPAGSLRCITCAVVGNGG
ILNNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFTAFSLTQSLLILGNRNGFKNVP
LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREALHMDRYLLLHPDFL
RYMKNRFLRSKTLDAHWRRIYRPTTGALLLTLALLCDQVSAYGFITEGERFSDHYYDTSW
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

DRAFT - 12526660

FIGURE 243

CG**ATG**CGGGACCCGGCACCCCCCTCCTGGGGCTGCTGCTGGTGCCTGGGCCCTCGCCG
GAGCAGCGAGTGAAATTGTTCCCTCGAGATCTGAGGATGAAGGACAAGTTCTAAAACACCT
TACAGGCCCTCTTATTTAGTCCAAGTGAGCAGCAAACACTTCATAGACTTATCACAACA
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAG**TGA**GCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCTTGGAAACCAACAGGGAAACAGAAACTATCTTATACACATCCCCTCATGG
ACAAGAGATTATTTTGAGACAGACTCTCCATAAGTCCTTGAGTTTGATGTTGTTG
ACAGTTGCAGATATATATTGATAAAATCAGTGACTTGACAGTGTATCTGCACTTATTT

244/330

FIGURE 244

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDCKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

FIGURE 245

GGGCTGGCCCCGCCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTGGGAGG
 CCCGACCCGGCCGCCAGCCCCCACCATGCCACCCGC~~GGG~~CCTCGCCGGGCCGCCG
 CTCACCGAATCGCTCTGTTGGTGC~~TGGGG~~CTCCCTGGTGC~~TGGCCGG~~GAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCTGGCATCCGGGTTAACTGCAGTTCTCACCTCT
 GCTGCGGGACCTGCTACCGTACTGCTGCAGGGACCTGACCTGCTTATCACCGAGAGG
 CAGCAGAACGACTGCCTGGCCCTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTGTGCTGTGGTGCCACCACCATCTGCTGCTCCTCTGTTGCTACCTGT
 ACCGCCGGGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGAGCCAGTATAACCCATACCCCCAGGACCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCCACTCTACCCAGCTGGGCC
 CAGTCTACAACCCCTGCAGCTCCTCCCTATATGCCAACACAGCCCTTACCCGGGAGCC
TGAGGAACCCAGCCATGCTCTGCTGCCCTTCAGTGTATGCCAACCTTGGGAGATGCCCTAT
 CCTGTACCTGCATCTGGTCTGGGGTGGCAGGAGTCTCCAGCCACCAGGCCAGACCAA
 GCCAACCCCTGGGCCCTACTGGGGACAGAGCCCAGGGAAAGTGAACAGGAGCTGAACTAGA
 ACTATGAGGGGTTGGGGGAGGGCTGGAATTATGGCTATTTTACTGGGCAAGGGAGG
 GAGATGACAGCCTGGCTCACAGTGCCTGTTCAAAATGTCCTCTGCCAACAGATCCAG
 CCAGGAAGGCTGGGCCCTACTGTTGTCCTCTGGCTGGGGTGGGGGAGGGAGGAGG
 TCCGTCAGCAGCTGGCAGTAGCCCTCTCTGGCTGCCACTGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTIAALLVLGAPLVLAGEDCLWYLDRNGSWHPGFNCEFFTFC CGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCA GTGGTGGCGGGCGCAAGGGTAGGGCGGCCAGAA
 CCCCAGGTAGGTAGAGCAAGAAG **ATG** GTGTTCTGCCCTCAAATGGTCCTTGCAACCATG
 TCATTTCCTACTTCTCAGTGTGGCTCTTAACTGTGTCACCTCCATGGGTGTCAGAG
 CACTGAAGCATCTAAAACGCTAGTGATGGACACCAATTCTTGAATAAAAATACGACTTC
 CTGAGTA CGTCATCCCCAGTTCATTATGATCTTGTATCCATGCAAAACCTTACCAACGCTGACC
 TTCTGGGAACACGAAAGTAGAAATCACGGCAGT CAGGCCACCGAACCATCATCTGC
 TAGTCACACCTGCAAGTCTGGCAACCCCCCTCACCGAACAAATTGCACTGCTGGCTCCCGAG
 AAGAACCCCTGCAAGTCTGGCAACCCCCCTCACCGAACAAATTGCACTGCTGGCTCCCGAG
 CCCCTCTGTGGCTCCCGTACACAGTTGTCATTCACTATGTCGAATCTTCGGAGAC
 TTTCCACGGGATTTCAAAAAGCTACAGAACAAAGGAAGGGAACTGAGGAATACTAGCAT
 CAACACAATTGAACCCACTCGAGCTGAATGGCCTTCCCTGCTTGTGACCATCGCTT
 AAAGGAAGTCTTCAGAAATTTCAAAATTAGAAGGAGGCCAAGGGCCTAGCCATCTCAATG
 ATTGGTGAAGATCTGACTGTGCTGAAGGACTCATAGAAGACCATTTGTGACTCTGTA
 AGATGACCCATCAGTGTGGCCTTCATCTTCAGATTGGACTGTGCAAGAACATAACC
 AAGAGTGAGCTAAGGTTCTGTTATGCTGTCACAGAACATAATGCAAGAACATAATTG
 ACTGGATGCTGCGTGACTCTCTAGAATTATGAGGATTATTTCAGCATACCGTATCCCC
 TACCCAACAAAGACTCTGCTGCTATCCGACTTICAGTCTGGCTATGGAAAGACTGGGA
 CTGACACATATAGAAGATCTGCTCTGTGTTGTGAGTCAGAACAGTCTTCGCACTAAGTA
 GCTTGGCATCACAGTACTGTGGCCCATGACTGGCCACAGTGGTTGGAACTGGTCA
 CTATGGAAATGGTGAATGATCTTGGCTAAATGAAAGATTGCAAAATTATGGAGTTGT
 TCTGTCAGTGTGACCCATCTGAAGAAGTTGGAGGATTATTCTTGGCAAAATGTTGA
 CGCAATGGAGTAGTGTCTTAAATCTCACACCTGTGTCACACCTGTGGAAACATTCTG
 CTCAGATCGGGAGATGTTGATGATGTTCTTATGATAAGGGAGCTTGTATTCTGAATATG
 CTAAGGGAGTATCTGCGCTGACGCAATTAAAAGTGGTATTTGACAGTATCTCCAGAACAG
 TAGCTATAAAAATACAAAAACGAGGACCTGTGGAGTAGTGTGCAAGTATTGGCCTCATAG
 ATGGTGTAAAGGGAGGGATGGCTCTGTGAAAGTCAACATCATCTCCATCAT
 TGGCATCAGGAAGGGTGGATGCTGAAAGACCATGATGAAACACTGGACACTGCAAGGGGTT
 TCCCCATAATAACCATCACAGTGGAGGGGAGGATACACATGAAGCAAGAGCACTCATG
 AGGGCTCTGACGGCCCCCGGACACTGGCTACTCTGGCATCTTCAATTGACATTGATC
 AGCAATCCAACATGGCCATCGATTGGCTAAACAAAACAGATGTGCTCATCTCC
 AGAAGAGGTGGATGATGCAATTAAATGTTGGGCTGATGAATGGCTATTACATGTGCT
 AGGATGATGGATGGAGCTCTTGTACTGCCCTTTAAAGGAACACACAGCAGTCAGCAGT
 AATGATCGGGCAACTCTCATTAATGACCTTACCTGCTGACGCTGGCATTGGGAAGCTG
 TGCAACACTATCGCCGTGCGTGCAGCTGACCTTGGCAGTGTGTGCTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTCTTATAGTTAATGGGAAAGAGGATGATGAATGAAGT
 GAAAGCTTAAGGGAGATAAAAACACTCAGGAGTTCCACAAATTCTACACTCATGG
 CAGGAACCCAGTAGGATACCCACTGGCTGCAATTCTGAGGAAAACCTGCAACAACTGG
 TACAAAGTTGAGACTGGCTCATCTTCATAGCCACATGGTAATGGGTACAAACATCAA
 TTCTCCCAAGAAACAGGCTGAGAGGTTAAAGGATTCTCAGCTTTGAAAGAAAATGG
 TTCTCAGCTCCGTGTGTCACAGAACATTGAAACCATGAAAGAAAACATGGTGGATGG
 ATAAGGATTTGATAAAATCAGAGTGTGGCTGCAAGTGGAAAGCTTGAACGTTGAT**TAAAAA**
 TTCTCCCTTGCCGGGTTCTGTATCTCTAATCACCAACATTGAAAGTGTGATTCTCAA
 ACTAGAGGATGGCTGTGTTGGCTCAACTGGAGATCTTCTTCCCTCAACTCTTGTG
 CTATCTCTGTGAAAGAATGCTGTGTTCTGATCACAGGTGTTGCCCTGCACTGAA
 TCCCTGCCACAGAACATAAGTACCTTATTCTCTCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSLLALLTVSTPSWCQSTEASPKRSRGDTPFWNKIRLPEYIVPVH
YDLLIHANLTLFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQLVLE
HPPQEIQIALLAPEPLLVLGPLYTWWIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
ARMAFPFCDEPAFKASFISIKIRREPRHLIASNMPLVKSVTVAEGLIEDHFDTVKMSTYLVA
FIISDFEVSKITKSGVKVSVAVPDKINQADYALDAVTLLEFYEDYFSIPYPLPKQDAA
IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTAHELAHQWFGNLTMEWWNDL
WLNEGFAKEMEFVSVSVTHPELKVGDDYFFGKCFDAMEVDALNSSHVPSTPVENPAQIREMFD
DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDMSASICPTDGVKGMDG
FCSRSHQSSSSSHWQEGVDVKTMNNTWLQRGFPLITITVRGRNVHMKQEYHMKGSDGAPD
TGYLWHVPLTFITSKSNSMVHRFLKTDTVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
TGLLGHTAVSSNDRASLINNAFQLVISGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
MYKLMERKRDNEVETQFKAFLIRRLRDIDKQTWTDEGSVSEQMLRSELLLLACVHNYPQCV
QRAEGYFRWKESNGNLSLPDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALC
RTQNKEKLQWLLDASFKGDKIKTQEFPQILTLIGRNPVGYPLAWQFLRKWNWNKLVQKFELGS
SSIAHMVMGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTIETIEENIGWMDKNDKIR
VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCA**TG**AGCGGGTATTACTGCTGGCCCTCCTGGGTTCATCCTCCCAC
 TGCCAGGAGTGCAGGCCGTGCTCTGCCAGTTGGACAGTCAGCATGTGTGAAAGGTGTCC
 GACCTACCCCGGAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGGCCCCGCTACTGAGCACCGATGGGCCCAGCCTCCCTGATC
 TCCTACACCTCGTGTGCCGCCAGGAGGACTCTGCAACAACCTCGTTAACCTCCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTGAGGTGCCAGTCTGTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGGCATCTTCTCAATCTGAGAGTCCAGGGATGCGATGCC
 CCAGGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGGCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTCTGACCTGTATCGGGGACCACATTATGACACACGGAAAC
 TTGGCTCAAGAACCCACTGATTCGACCATCGAATACCGAGATGTGCGAGGGGGCAGGT
 GTGTCAGGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGACAAAAG
 GCTGCAGCACTGTTGGGCTCAAATTCCAGAACGACCACTCAGCCCTCTGG
 GTGCTTGTGGCTCTATACCCACTCTGCTCCTCGGACCTGTGCAATAGTGCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCTCAAGCTGCCCTGTCCCAGGAGACGGCAGTGT
 CTACCTGTGTGCAGCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCTAGG
 GGCAGCACTCATTGTTATGATGGTACATTCTCATCTCAGGAGGTGGCTGCCACCAAAAT
 GAGCATTAGGGCTGCGTGGCCAACCTTCAGCTTGTGAACCACACAGACAAATCG
 GGATCTCTGCGCGTGAGAACGCTGATGTGCGACGCCCTGCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCAGTTGGGGGTGGGCTGGCACTGGCCCAAGCGCTGTG
 GTGGGGAGTGGTTGGCTCTGCT**TAA**CTCTATTACCCACGATTCTCACCGCTGTGA
 CCACCCACACTCAACCTCCCTGACCTCATAACCTAATGGCCTGGACACAGATTCTTC
 CCATTCTGTCCATGAATCATCTCCCCACACAACTCATTCTACACCTAACAGCA
 AACACTGGGAGAGCCTGGAGCATCCGACTGCCATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCTGTCTTCA

FIGURE 250

MSAVLLIALLGFILPLPGVQALLCQFGTVQHVKVSDLPRQWTPKNTSCDSGLGCQDTLMLT
ESGPQVSLVLSKGCTEAKDQEPRVTTEHRMGPGLSILISYTFCRQEDFCNNLVNSLPLWAPQP
PADPGSLRPCPVCLSMEGCLEGTTEEICPKGTTCHYDGLLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFTCHRGTTIMTHGNLAQEPTDWTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTCSTVGAQNSQKTTIHSAAPGVLVASYTHFCSSDL CNSASSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSGS PRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACCCCCCGTTCGCCTAGCGCGTGCCTCAGGAGTTGGTGTCTGCCTGCCTGCCT
 CAGG**ATG**AGGGGGAAATCTGGCCCTGGTGGCGTTCTAATCAGCCTGGCCTTCCTGCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGATGCGGGAGAGAAGGGAGACAAAGGCCCGGACGGCCTGGAAGAGTCG
 GCCCCCACGGGAGAAAAGGAGACATGGGGACAAAGGACAGAAAGGCAGTGTGGTCGTCACT
 GGAAAAATTGGTCCCATGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAAGGCCCTCCCATGTGAGTGAGCCAGCTGCGCAAGGCCATGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTCGCC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAACGCCTACGCC
 CGCCCCAGCTGTCTGCCAGGGCCGCCGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCC
 ATGGCCTGATGGCCGCATAACCTGGCGCAAGCCGGCTGGCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGCCCTCGTGTACTCTGACCACTCCCCATGCGGACCTTCACAA
 GTGGCGCAGCGGTGAGCCAACAATGCCCTACGACGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGCTGGAACGACGTGGCTGCCACACCACCATGTAACCTCATGTGAGTTGACAAG
 GAGAACATG**TGA**GCCTCAGGCTGGGCTGCCATTGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGGCCAGGGAGCTGTCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTCTAAACTGAGAAAATGCCCTATGCTTAAGAGGAAAATG
 AAAGTGTCTGGGTGCTGTCTGAAGAACGAGTTCAACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTTCCATAAGCTGTGCCTTGTCCAAGC
 TATACAATAAAATCTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAA

FIGURE 252

MRGNLALVGVLISLAFLSLLPSGHQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGDMGDKGQKGSGVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQILSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFFIGINDLEKEGAFVYSDHSPRTFNKWRSGEPNNAYDEEDCVERMAS
GGWNDVACHTTMYFMCEFDKENM

FIGURE 253

AGTGACTGCAGCCTTCTAGATCCCCTCACTCGTTCTCTCTTCAGGAGCACCGCAG
 CACCACTGTGTGAGGGGAGCAGGCAGCGTCTAGCCAGTCTGATCCTGCAGACCACC
 CAGCCCCGGCACAGAGCTGCTCCACAGGCACC**ATG**AGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCCTGGGGGGCGCAGCAAGAGGGATCCAGATCTACAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTGGAGGGATTGCTCAAAGCCCTGAGGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCGAGAACGTCAGATGCATGACTCTTGTGGACTATGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTACCTTCAGTGAGGGTCCCTCGGCC
 CTTCATCCAATCAGCTGGATCCACAGGAAAGTCTCCCTGGAACAGAGGGCAGAGACC
 TTTA**TAA**GACTCTCCTACGGATGTGAATCAAGAGAACGTCCTCAGCTTGGCATCCTCAAGT
 ATCCCCCGAGAGCAGAATAGGTACTCCACTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCTGCTCCAATCCCCAGGTGCGCACGCTCTGTTACCTTCTCTTCCCTGTTCTG
 AACATTCTGTGCTTGACTCTTCACATCTTCTACCTGACCTGGGTGTGGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGCATTGACTGTAGAATACCTAGAGTCTGTACTGT
 CCTACATTTAAAAATAATGTCTCTCTATTCCCTAACAAATAAGGATTTGCAATATGAA
 AA

FIGURE 254

MRIMLLFTAILAFSLAQSGAVCKEPQEEVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHFFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGCGCTCCGGCTGCTCTATTGAGCTGTCGCTCGCTGTGCCGCTGTGCCCTGCTGTGCC
CGCGCTGTCGCCGTGCTACCGCGTCTGGACGGAGACGCCAGCAGCTGGTATTG
GAGCCCTGGAGAGCTCAAGGCCAACCTCTGCCCCAGGAGCCCAGGCTGCCCTGAGTC
CCATAGTGTGCTGAGGAGTGGAGCCATGAGCTGCGTCTGGTGGTGTATCCCCCTGGGGC
TGCTGTTCTGGTCTCGGATCCAAGGCTACCTCTGCCAACGTCACTCTCTTAGAGGAG
CTGCTCAGCAAATACCAGCACAAACGAGTCTCACTCCGGTCTGCAGGCCATCCCCAGGGA
GGACAAGGAGGAGATCCTCATGCTGCACAAAGCTTCGGGGCAGGTGCAGCCTCAGGCCT
CCAACATGGAGTACATGGTGGCGCCGGCTCCGGCCAGAGGCTGCCACGGGGCTGGGGC
CTGGGCCACCCAGCCTGCTCTGTTCCCAAGCCAGCTCTGTTCCCAGGCCAGTGCCTGTGATGG
CTGGCTCAGGGTCTCTCTGGCAGGGGAGGATCCGGCTCTGTTCTGTTTGTGTTGTTGTT
TTGAGACAGGGTCTCACTCTGCCACTGAGCTGGAGTCAATGCCAACATGTCATGCCCTG
AAACCTTAGACTCCCGGGTTAAGCGATCTGCTCAGCCTCCAAGTAGCTGGAACACAG
GCATGCACCATGGTGCCTCAGCTAGATTAAATATTGTGGAGATGGGGTCTGCTACGT
TCCCCAGGCTGGTCTGAACCTCTAGGCTCAAGCAATCCTCTGCCCTCAGCCTCTAAAGTG
CTAGGATTATAAGGATGAGTCACCCCTGTCGGCTCTGGCTCTGTTCTAACATTGCCCCAA
ACAACACACGTGGTCTCTGTGCAGAGCCTGCCCTGGCTCATGTCACCTTGGTAGC
TCCACTGGAAACACAGCTCTGCCCTTCCACCTGGAGGCAGATGGGGAGGGGGCCAGGG
CTGGGCTTGTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCCCTGACTCTC
CTTAGCCCGTGTGAGCCTCACTTCCACTTGGAGACTCTCTGCCGTGGTGCCTGACT
GTGAGATAAGTCAGGGCTGTGAAGGGCCGGCACAGACTGACCTGCTCCCCAACCCCTAGG
CTTGTCAACCGGGAAAGGAGCTAACGGTACAGAAAGACAGCCAAGGTCAACCCCTCCGGGT
GATTGTGATGGGTGTTCCAGGTGTGGTGGCGATGCTGCTACTGACCCCAAGCTCCAGT
TGGAAACTCTCTGGCTGGTTTCCAGAACACTACAGAGGAATGGACCAAGCTTCCAGG
GTCCCTCTCGTCCACCAACCGGGAGCCTGCCACCTGGCCATCGTCAGCTATGAATGGCTT
TTAAACAAACCCACGCTCCAGCCTGGTAACATGGTAAAGGCCGCTCTACAAAAAAATC
CAAGTTAGCCGGCATGGGGTGCACCTGAGTCCAGCTGCAGTGGGAGTGGAGGCTGAGGCTG
GTGGAGGTGGGGGGTGGAGCTGAGGAAGGAGATGCCCTGAGCCTGGGAAGTGCAGGCTG
AGTGAAGCTGAGATTGACCAACTGCACTCCAGCCTGGTGCAGAGCAAGACCCCTGTCAAAAA

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FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLEELLSKYQHNESHSRVRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWLGHQPALFSQLCSPASACDGWLVRSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKE

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

PDB ID: 1Z2525660

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGG
GTCTGGGCTGCCCTTGCTCTCTCTTGACCCCTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTGCAACTGAAGCTGAAGGAGTCTTCTGACAAATTCTCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCCTCCATCTCCCTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTG
TGTCCCTTCTGGCCCGGGCTTTGGCCGGGATGCAGGAGGCAGGCCCGACCCTGTCTT
CAGCAGGCCACCCCTGAGTGGCAATAAAATTCGGTATGCTG

FIGURE 258

MGSGLPLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLAKLCLLHLPSGTS
VTLHHARSQHHVVVCNT

09992521.111401

FIGURE 259

AATTGTATCTGTAAATGTTAAAACAAACGAAATAAATAGAAGGAAAAACTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTAAACAAATTAACTGTTAGGATTGCAGT
TATGATTGGATATTAAATTCTGTTCTGATGTGGGGTTCTCCACTGTGTTCTGTGTC
TATTAATATTTACCATTCGAGCAGCTTCATTCACTGTTGAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTCCTAATCAATGCAGAGTCCCTCCC
CTCCGATTGTTCTAAAT**AA**TTGAAAGATGTCGCTGTTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCCTTGTGGAAAGGTCTTGAAAGCCAATGGAATACTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTACCTTCACTTAGTAGGATGTGTTACGCTA
GTAAAATAGAAACCTGTGTTATTCTCAGGTATTTAGAAACAAACAGCCATCTTTATTTT
ATGTGTGTTCTGGCTGTATTCTAAATTATATTTGGCTATCAAATATTCTCAT
TCAATATAAATAACAATAGTAGAAGTTACTTAGATATGCTTCTAGTTGCATTTCTC
AGCCTATGTAAGACTACTTGTGAAATGCCCTGAAATTACAGTACTGTCCTCTACTA
TCTTCAGATTACTTGATTCAAATAACCAATTATGTTGTAATTGATATTAATAACCA
ATAAAAGTTCATATCTACCC

260/330

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

0999252661 • 111481

FIGURE 261

GAGGGATTGCCACAGCAGCGGATAGAGCAGGGAGAGCACCAACCGGAGGCCCTTGAGACATCCTT
 GAGAAGGCCACAGCATAAGAGACTGCCTGCTGGTGTTCGCAGGAT**ATG**ATGGTGGCCCTT
 CGAGGAACCTTCTGCATTTGCTGGTTCTGTCCTTGCAAGCTTTCTGCCCGCCGCAGTGTAC
 CCAGGACCCAGCCATGGTCATTACATCTACAGGCCCTTCGAGTCTTGAGCAAGGCTGG
 AAAAATGTAACCAAGCAACAGGGCATACATCAAGAATTCCAAGAGTTCTCAAAAATATA
 TCTGTCATGCTGGGAAGATGTCAGACCTACAAACTGAGTCAAAGAGTGCAGTGGTAACCTT
 GCCACTGAGAGTTAACGTCGCCAACGGGAGATTGAGTACATACATAACCTTCAGAGGCTG
 ACGAGTCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAGATCCGAGACTCTGCTGAAGCTGCAGAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACATGGCTTCTGGATGAAAGATGCTGTCTATA
 ACTCTCAAAGGTGACTTATTAAATTGGATCCAGAACAAACACTGTTGGAAATTGCAAAC
 ATACGGCATTATGGAGGAAACCCAAGCAGTCCCGGAGAACATCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGCATCTAACAAAGGTTTCTATTTTCTATAACCAAGCAACTT
 CTAATGAGATAATCAAATAAACCTGCAAGAGGACTGTGGAAAGATCGAAATGCTGCTCCCA
 GGAGGGTAGGCCGAGCATTTGGTTTACAGCACTGGCCCTCAACTTACATTGACCTTGGTTCTCA
 GGATGAGCATGGGCTTGGGCACTTACACTGGGCCAGGCACCCATAGCCATTGGTTCTCA
 CAAAGATTGAGGCCACACTGGGAGTGGAGCAGTGGGATACCCCATGCGAGAACGCCAG
 GATGCTGAAGCCTCATCTCTGGGGTTCTCTATGTTGCTACAGTACTGGGCCA
 GGGCCCTCATGCATCACCTGCATCTATGATCCACTGGCACTATCAGTGGAGGAGCTTGC
 CCAACTGTCTTCCCAGAACAGACAAAGTCACTCCATGATCCATTACAACCCCCAGAGAT
 AAGCAGCTTATGCCGATGAAAGAACAGATCATTTACAAACTCCAGACAAAGAGAAA
 GCTGCCCTGAAG**TAA**TGATTACAGCTGTGAGAAAGAGCACTGTGGCTTGCAGCTGTC
 TACAGGAGACTGAGGCTATAGCCCCCTTCAAAATAGTACCCCTTAATCACACACAGGAA
 AGTGTGTAAGATGGAAGAACATGATGCTTCTTCCAAAATGCACTGCCATTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTCAACAAATGCTTACAGGCTTAC
 CCTCTGGCTTCAAGGATGCCACATTCTGATACAGCTACTTCAAGCCATTGTGTTTACT
 GCTCCCAGCATTTACTGTAACTCTGCCATTCTCCCTCCCAACAAATTAGAGTTGATGCCAGC
 CCCTAATATTCAACACTGGCTTTCTCTCCCTGGCCTTGTGAAGCTTCCCTCTTCTT
 CAAAGTGTCTTGTATCTCCCATTTCTACTGCCAAACTTAAATACTTAAATTTCTT
 CTTTCTTCTTCTTGTGAGACAAGGTCTACTATGTTGCCAGGCTGGTCTCAAACCTC
 AGAGCTCAAGAGATCCTGCCCTCAGCCTCTAAGTACCTGGGAGATTACAGGCCAC
 CACACCTGGCTTAAATACTTCTTATTGAGGTTAACCTCATTTCCCTAGCCCTGTC
 CTTCCACTAAAGCTGGTAGATGTAATAAAAGTGAAGATATTAAACATTGAAATATGCC
 CCAGGGTGGAGGTGTTGCACATCATTGAAATTCTCGTTTACCTTGTGAAGACATGCCAAG
 TCTTTCAGCTGTCTTCTAGAGTTAGGTGAGTAACACAATTACAAAGTGAAGATACAGC
 TAGAAAATACTACAATCCCATACTGTTTCCATTGCCAAGGAAGCATCAAATACGTATGTT
 TGTTCACTTACTCTTATAGTCATGCCCTCATGTTTCAAGCCTTAAATAGTCTGTCCC
 TTAGCAGTTTCTGTCGCCAACAGACCTTCAATAGGCTTCAAAATGATAATTCTCC
 AGAAAACCAGTCTAAGGGTGAGGACCCAACTCTAGCCTCCTCTGCTGCTCTGT
 TTCTCTTCTGTTAAATCAATAAAAGTGACACTGAGCAAAAAAA

FIGURE 262

MMVALRGASALLVLFLAALPQQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRQCQTSEYKSAVGNLALRVERAQREIDYTQYLREADECIVSEDKTLAEMLL
QEAEEEKKIRTLLNASCDNLMGIKSLKIVKKMMDTHGSMWKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEIPTGLVEHESWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGQNIIYKLQTKRKLPLK

FIGURE 263

GGGCCCGGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC **ATGGAGCTCTCGCAGA**
 TGTCGGAGCTCATGGGGCTGTCGGTGTGCTTGGCTGCTGCCCTGATGGCGACGGCGGC
 GTAGCGGGGGTGGCTGCGCGGGGGAGGAGAGGGAGCGCCGGCCCGCTGCCAAAAGC
 AAATGGATTTCACACCTGACAATCTCGGATCCAAGAACAGAAACAAATATCAGCGGATTC
 GGAAGGAGAACGCTACAACAACACAACCTCACCCACCGCTCTGGCTGAGCTGAAGAGC
 CACAGCGGAACATATCTGCATGGACTTAGCAGCAATGGCAAATCTGGCTACCTGTG
 AGATGATCGCACCATCGCATTGAGACCAAGGACTCTCTGCAGCGAGACCCAGAGCA
 TGAGAGGCCAACAGTGGAGCTGGACCACGCCACCCCTGGCTGCCTCAGCCCTGACTCGAGAGCC
 TTCATCGTCTGGCTGGCAACGGGACACCCCTCCCTGGCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGTACACCTCACAGGCCACCCAGAGGACTCCCTAAAAGCACAAGGCCTGTCA
 TCGACATGGCATGGTCAACAGGAGTTATCATGCTCCAGTGCCTCCAGTGCACACCATTGTC
 CTCATCTGGAGGCTGAAGGGTCAAGTGTCTACCATACAACCAACAGATGAAACACAC
 ACACGCTGTTGATCTCCCTGGAGATTGTAGCCTCGTGTGCTTCACCCAGATGTGA
 AGGTTTGGAAAGTCTGTTGGAAAGAAGGGGAGTCCAGGGAGTGGTCCGGACCTTGAA
 CTAAAGGCCACTCCGGGCTGCACTCGTTGCTTCCAAACGACTCACGGAGATGGC
 TTCTGTCCTCAAGGATGGTACATGAAACTGTGGGACACAGATGGAATAACAAGAAGC
 AGGACCCACTTGCTGAAGACAGGGCGTTGAAGAGGCGCGGGTGCGCCGGTGC
 CTGGCCCTCTCCCCAACGGCCAGGTTGGCCAGTGCAGTAGTATCTCATCTA
 CAATACCCGGGGGGGAGAAGGGAGATGCTTGGCCAGTGCAGTAGTATCTCATCTA
 ACTTGTCTTTGACATCAGCCGCTTCTGGCTCCCTGTGGGACCGGGCGTGC
 TTTCAACACACTCTGCCACGGCCATGGTGGAGGAGATGCAAGGGCCACTGAAAGGGG
 CTCCAAACGAGACCCGGCAGAGGCGCAGCAGCTGACCCAGGCCCCAAGAGACCTGA
 AGAGCTGGTGGCTGAGAACAGTCAACTCTGGAGGGCCCGCCAGAGGATTGAGGAGGAG
 GGATCTGGCTCTCATGGCACTGCTGCCATCTTCTCCAGTGGAAAGCCTTCAAGAGG
 AGTCTCTGGTTTCTACTGGTGGCTCTTCCATTGAAACTACTCTGTCTACTT
 AGGTCTCTCTCTCTGGTGTGACTCTCCCTGACTAGTGGCCAAGGTGCTTTCTC
 CTCCAGGCCAGTGGTGGAACTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGGAG
 AGGAGAGAGAGAGAATGTGATTGGCTTGTGGCAGCACATCCTCACACCCAAAGAAG
 TTTGTAATGTTCCAGAACACCTAGAGAACACCTGAGTACTAACAGCAGTTTGCAGA
 TGGGAGACTGGGATACCTCCCATCACAGAACTGTGTTCCATCAAAAGACACTAAGGGATT
 TCCTCTGGGCTCAGTCTATTGTAAGATGGAGAATAATCCTCTGTGAACCTCTGCA
 AAGATGATATGAGGCTAAGAGAATACTAACGCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
 AGTACTATTGTCCTGGAAAGTGGTAAAGTGGGAACCACTGTGCTTGAACCAAAAA
 TTGAAACACATCTCTGGAAAGGCAAAGTTCTGGACTTGATCATACATTATGTT
 TGGGACTCTCTCTGGAGATGATATCTGTTAAGGAGACCTTTTCAAGTCATCAAG
 TTCATCAGATATTGAGTGGCCACTGTGCCCCAATAAATATGAGCTGGGGATTAAAAAA
 AAA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQRIRKEKPQQHNFTHRLAALALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHTATLVRFSPDCRAFIIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTP DVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVKDGTVKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAACRCLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGRDRAVRLFHNTPGHARAMVEEMQGHLKRASNESTRQLQQQLTQ
AQETLKLKGALKK

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAACAGG
 CAGTGTGTTGCCCTCACCCCAAGTGACC**ATG**GAGGGTGCACCGAGTCATCATGCTCC
 TCCTAGTAACTGTGTCGTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTCGAGGGCTGCAGGATGTGCACCCCGCT
 GGGGCGGGAAAGGCAGAGTGCACCCGGCAGCCACAAGGTCCCTTCAGGAAACGCA
 AGCACCAACACTGTCTTGCTGCCAACCTGCTGTGCTCCAGGTCCCGACGGCAGGTAC
 CGCTGCTCATGGACTTGAAGAACATCAATT**TAG**CGCCTTGCTGGTCTCAGGATAACCA
 CCATCCTTCTGAGCACAGCCTGGATTTCATTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCCAAGTCCCTACACTGACTACCCCTGATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
 CTGTGGTGTGAAAGGGCCAGCCTGGTCTCTCCCTGCTCAGGCTGCCAGAGGGTGGTA
 AATGGCAGAAAGGCATTCCTCCCTCCCCAGGTGACCTCTCTCTTCTGGCCCTG
 CCCCTCTCCCCACATGATCCCTCGCTGTAATTAGACATTCTGGCACAGGTCTGGT
 GCATTGCTCAGAGTCCCAGGTCTGGCCTGACCCCTCAGGCCCTCACGTGAGGCTGTGAGG
 ACCAATTGTGGTAGTTCATCTCCCTGATTGGTAACTCCTAGTTTCAAGACCACAGAC
 TCAAGATTGGCTCTCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAAGGGAGCCA
 GGGAGGCAATCAGCCCCCTGAAGACTCTGGTCCAGTCAGCCTGTGGCTTGGCCCTGTGA
 CCTGTGACCTCTGCCAGAATTGTCATGCCCTGAGGCCCTCTTACACACTTACAGT
 TAACCACGTAAAGCCCCAATTCCACAGCTTCCATTAAAATGCAAATGGTGGTGGTCAA
 TCTAATGTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTAAACAACCTCGTTCCA
 AGGATCAGCCCTGAGAGCAGGGTGGTGAATTGAGGGAGGCCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTCAAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTACAATAAAAGCACCACACTGAAAAAA

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FIGURE 266

MRGATRVSIMLLLTVSDCAVITGACERDVQCGAGTCCAISLWLRLGLRMCTPLGREGECHP
GSHKVPFFRKHKHTCPCLPNLLCSRFPDGRYRCSDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCGGGCGTCGGGGCGGTAAAAGGCCGCAGAAGGGAGGCACTTGAGAAATGTCTTTC
 CTCCAGGACCCAAGTTCTTCACCATGGGATGTGGTCCATTGGTGCAGGAGCCTGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCAACACAGACGTGTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAACCAAGGAAGTTCAAA
 GCAAAGGAGCTATGGAAAAAAATGGAGCTGTGATTATGGCCGTGGAGGCCAGGCTGTTT
 CCTCTGTGAGAGGAAGCTGCGGATCTGCTCTCCCTGAAAAGCATGTTGGACCAGCTGGGC
 TCCCCCTCTATGCACTGGTAAAGGAGCACATCAGGACTGAAGTGAAAGGATTCCAGCCTTAT
 TTCAAAGGAGAAATCTCCTGGATGAAAAGAAAAGTCTATGGTCCACAAAGCGGAAGAT
 GATGTTATGGGATTATCCGCTGGAGTGTGTTACAACCTTCCGAGCCTGGAACGGAG
 GCTTCTGGAAACCTGGAAGGAGAACGGCTCATCCTGGGGAGTTCTGTGGTGGATCA
 GGAAAGCAGGGCATTCTCTTGAGCACCGAGAAAAAGATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAAATGA
 TGTGTGAAACTGCCAGCTCAGGATAACCAGGGACATTACCTGTGTTCATGGGATGTATT
 GTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTAATATTCTGTTAGGCCACTAAGGAAAATAGCCCCAAACAAAGACTGA
 CAAAAATCTGAAAAACTAATGAGGATTATAAGCTAAACCTGGAAATAGGAGGCTTAAA
 TTGACTGCCAGGCTGGTGCAGTGGCTCACACCTGTAATCCCACACTTGGGAGGCCAGG
 TGAGCAAGTCACTTGAGGTGGAGTTCGAGACCGCCTGAGCAACATGGCAGGCCCCGTC
 TCTACTAAAATACAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCAGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKAALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCG
GGCCAGGTGCCCGTCGCAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGCGAGCGCGAGA
AGCCCCTTCTCGCGCTGCCAACCGCCACCCAGCCC**ATGGCGAACCCGGCTGGGCTG**
CTTCTGGCGCTGGGCTGCCGTTCTGCTGGCCCGCTGGGCGAGCCTGGGGCAATA
GACCACTCTGCAAATGAGAATAGCACTGTTTGCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCCTCCCTCTGGCTGCCTG
CTCCTGGCTGTGGGCTGGCACTGTTGGTGCAGCTCAGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCATGCAGCCAGGCCGGCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCAT**CAGTCCCCCTCCTGCATCTGTCTCC**
CTTCATTGCTGTGTGACCTTGGGAAAGGCAGTGCCCTCTCTGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTATATTTATATAAAATTAGTACTGAGATGTAAAAAAAAAAAAAAA

FIGURE 270

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSSSSDGNLRPEAITAIIV
VFSILAAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

FIGURE 271

AATATATCATCTATTATCATTAAATCAATAATGTATTCTTTATTCCAATAAACATTGGGTT
TTGGGATTTAATTTCAAACACAGCAGA**ATG**ACATTTCCTGTCACTATTATTGTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTAGGAAGCAACACATTGGAGAATGGCTACTTCT
ATCAAGAAAATAAGAGAACACAGTCACCCACACAATCATCTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACACCAGGCAAGGCATAGTTAAAGGACGGAATCTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGCAGGGGTGAAAGAAAAACACT**TAG**ATTCAATG
ATTGTAAATTAAAGGCAAATACACATATTAGTATTACCTTAGTGTAAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCATGCACTGGCTGGACAGTTCAAATTGGACT
TTATTAATTAAACAGTAACGTGATTACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTGATAACAAATAAGAAAAGTGTCTCTCCCCTACAGAATTGACATTAA
ATGCGATAACAGTTAGAAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGAAAATGTTGCCAAGGAAAAAA

FIGURE 272

MTFFLSSLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

FIGURE 273

GCCAGGAATAACTAGAGAGGAACAA**TGGGGTTATTCTAGAGGTTTGTTCCTTAGTTCTGCTGCTGCAACCAGTC**AAACTCTCATTAAAGCTGAATAATAATGGCTTGAAAGATA
 TTGTCATGTATTAGATCCTAGTGTGCCAGAAGATGAAAATAATTGAACAAATAGAGGAT
 ATGGTACTACAGCTTCACTGTGTTGAAGGCCAGAAAAAAGATTTTTCAAAA
 TGTATCTATTAAATTCTCTGAGAATTACCTCTAGTACAAAAGGCCAAACATG
 AAAACCATAAACATGCTGATGTTAGTGTGACCAACTACCTCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTCACAGAATGTGAGAAGAAGGCCAAACATTCACITCACCCCTGACCT
 TCTACTTGGAAAAAAACAAAATGAATTGCAACCCAGGCAACACTGTTGTCATGAGTGGG
 CTCACCTCGGTGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTCTAAG
 TCAAAAAAAATCGAACAGCAACAGGTGTCGGAGACTATCTCTGTTAGAATAGAGTTATAA
 GTGTCAGGAGGAGCAGCTGCTTGTAGTACAGCATGAGAATTGATCTACAAACAAACTGTATG
 GAAAAGATTGTCATTCTTCTCTGTAAGTACAAAACAGAAAAGCATCCATAATGTTTATA
 CAAAGTGTGTTGATGTTGAAATTTGCAAGAAAACCCATAATCAAGAAGCTTCAAG
 CCTACAAACATAATGCAATTAGAAGTACATGGAGGTGATTAGCAATTCTGAGGATT
 TTAACAAACACATACCCATGGTGCACACCCCTCTCACCTGTCTTCTCATGTCAGGATC
 AGTCAAAAGATTGTCGTTAGTCTCTGATAAGTCTGGAAAGCATGGGGTAAAGGACGCC
 AAATGATGAAATGAAACAGCAACAGTCTCTGTCGACAGACTGTTGAGACTGATCTGG
 TGGGGATGTTCACTTGTAGTACTGCCCCTATGTTAAATACTGAAATCCTAAATAAAAGC
 AGTGTGAAAGAACACACTCATGGCAGGATTACCTACATATCTCTGGAGGAACTCCAT
 CTGCTCTGAAATTAAATGATCTTCAGGTGATTGGAGAGCTACATTCCAACTCGATGGAT
 CGGAAGTACTGCTGACTGATGGGGAGGAAACACTGCAAGTCTTGTATTGATGAAGTG
 AAACACATGGGGCTATGTTCTATTGTTGCTGGAGAGCTGCTGATGAAGCAGTAAT
 AGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTTTCAGATGAAGCTCAGAACATG
 GCCTCATGATGCTTGGGGCTCTCATCAGGAAATACTGATCTCTCCAGAACAGTCC
 CAGCTCGAAAGTAGGGATTAAACACTGATAAGTAACTGCTCTGGATGAAACGACACTGCT
 TGATAGTACAGTGGGAAAGGACAGCTCTCTCATCAGGAAACAGTCTGCTCCAGTA
 TTTCTCTCTGGGATCCTGGTACAGGAAATAATGGAAATTCTCACAGTGGATCAACT
 ATGGCCTATCTCAGTTCCAGGAACATGCAAGGTTGGGCACTTGCCATACAATCTTCAAGC
 CAAAGCGAACCCAGAAAATTAACATTACAGTAACTCTCTGAGCAGCAATTCTCTGTG
 CTCCAACTCACAGTGAATGCTAAATGAATAAGGAGCTAAACAGTTCCCCAGCCAAATGATT
 GTTCTACAGGAGAAATTCACAGGATATGACTCTGGTCTCTGGGACCAATGTGACTGCTTCT
 TGAATCACAGAATGGCACATACAGGATTGGAACATTGGATAATGGTGCAGGGCCTGATT
 CTTTCAGAATGATGGAGTCACTCAGGTATTTCAGCAGTACAGAAAATGGCAGATAT
 AGCTTAAAGAATGATGGAGTCACTCAGGTATTTCAGCAGTACAGGCTAAATTAGCCT
 GAATAGAGCGCGTACATACCAGCTGGGTAGTGACCGGAAATGTGAGCAGAACCCGCC
 GACCTGAAGATTGATGGAGTACTCAGAACCTGGGAGGATTTCAGCCGAACAGCATCCGG
 GGTGCATTGTTGATCACAAGTCCAAAGCCTCCCTGGCTGACCAATCCCCACCAAGTCA
 AATCACAGACCTGGATGCCACAGTCAGGAGATAAGGATTCTTACATGGCACAGCACCAG
 GAGATAATTGATGTTGGAAAAGTCAACGTTATACTCATAAGAATAAGTGCAGTATTCTT
 GATCTAAGAGACAGTTGATGATGCTCTCAAGTAATAACTACTGATCTGTCACCAAAGGA
 GGCCAACTCCAAGGAAAGCTTGGTACATTTAAACAGAAAATCTCAGAAGAAATGCAACCC
 ACATATATTGCCATTAAAGTATAGATAAAAGCAATTGGACATCAAAGTACATCCACCAATT
 GCACAGTAACTTGTATTCTCTGATAAAAGTCATAATTCTGGAGTTAATATTCTACGCTGTTAT
 TACTCTACTCCTACTCTGATAAAAGTCATAATTCTGGAGTTAATATTCTACGCTGTTAT
 TGTCTGATGGGTCTGTTAATTGTAATTCTTAACTTATTTAAAGTACCCATT**TGAACCTTA**
 ACGAAGAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAACAAACAACTGTAAGT
 AAAGGATATTCTGATCTTAAACATCCCATGTTGATCATAAACTCATAAAATAATT
 TTAAGATGTCGAAAAGGATACTTGTATTAAATAAAACACTCATGGATATGTAAC
 CAAGATTAACATTAGTTGTTATTGTTATTGTAAGGAAATAGTGTGAC
 AAAGATCCTTTCTCATGATACCTGGTTCTATTGATGTCACAGTTTCTGAAAT
 GATATTCAAAATGCAAGAAATTAAACATCTATGAGTACTGAGTAC
 GGAGAGCAATAAACACATTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 274

MGLFRGVFVLLVLCLLHQSNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENKHADIVAVAPPTEPDKQFTEC
 GEKGEYIHFTPDLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNICKCNFRSTWEVISNSEDFKNTIPMVTPPPPVSLLKISQRIVCLV
 LDKSGSMGGKDRLNRNMQAAKHFLQLTVEENGWSWGMVHFSTATIVNKLIQIKSSDERNLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSVELLTDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKitGGSHFYVSEDAQNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNNDGVYSRYFTAYTENGRSLKVRAGH
 GANTARLKLRRPLNRAAYIPGVWVNNGEIANPPREIDEDEDTQTTLEDFSRTASGGAFVVSQV
 PSLPLPLDQYPPSQITDLDATVHEDKIIILTWTAPGDNFDVGKVQRYIIRISASILDRLDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
 QANPDDIDPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

TOP SECRET 1252660

FIGURE 275

FIGURE 276

MMMVRRGLLAWISRVVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRYVSSLKRQIAQLKEELQERSEQLRNGQQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDSTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIESALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYEFTFKGDHKHEFKRLILFRPFSPIMKVKNEKLNMANTLINVIVPLAKRVDKFQRQFMQNFRREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIIYGHHDAVPPLLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLIDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGFLFHLWHEKRCMDELTPEQYKCMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQTSSKKT

FIGURE 277

FIGURE 278

MLWLLFFLVTAIHAEQCQPGAENAFKVRSLIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NCREATEISHVLLCNVTQRVSFWFVVTDP SKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLE
FLKIPSTLAPPMDPSVPWIWIIIFGVIFCIIIVAIALLILSGI WQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGLMMPS

FIGURE 279

AACTCAAACCTCTCTGGAAAACGCGGTGCCTGCTCCTCCGGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCGTCCGGCTCTGGGCAAGGCTGGGTTCCCT**ATGT**
 ATGGCAAGAGCTACTCGTCGGTGCTCTCCCTGGCATACAGCTCACAGCTCTTGG
 CCTATAGCAGCTGTGGAAATTATAACCTCCCGGTCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAATGCACCTTCTCAGCTTGCCTGTTGGGTGATGCTCTAACAGTGACCTGG
 ATTTCTCTCTAGACGGGGGACCTGAGCAGTTGATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGGGTTAAGGACCGGGTGTCTGGATGGGATGGGATCCTGAGCGGTACGA
 TGCCCTCCATCCTCTGGAAACTGCAGTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGATAGGGGAGATCCGGCTAGCGTCGTGACACTGTA
 CGCTTCTCTGAGATCCACTTCTGGCTCTGGCATTGGCTCTGGCTGTGACTGATGATCAT
 AATAGTAATTGTTAGTGGCTCTTCCAGCATTACGGAAAAAGGGATGGGCGAAAGAGCTC
 ATAAAGTGTGGAGATAAAATCAAAGAAAGAGGAAAGGCTAACCAAGAGAAAAAGGTCTCT
 GTTTATTAGAACACAGAC**TAA**CAATTAGTGGAGCTGAGATGATTCCAAGAACAA
 GAACCCTAGTATTCTGAAGTTAATGGAAACTTTCTTGGCTTCCAGTTGTCAGCCGT
 TTTCCAACCAGTTCTGCAGCATATTAGATTGACAGCAACACCCCTCTGGAGGCCAGCAC
 AGTGCTCCCTCATATCACCAGTCATACACAGCTCAATTAAAGGTCTTATTAAATTCTAGA
 GTGTAATTCTTCAAGTGCCTATTAGGTTTATAAAACAAGAAGCTACATTGCTCCCTTAA
 GACACTACTACAGTGTATGACTTGTATACACATATATTGGTATCAAAGGGATAAAAGCC
 AATTGTCTGTACATTCTTCACTATTCTTCAAGTATTCTTCACTGAGCACTCTGCTACTAAAGTTA
 ATGTGTTTACTCTTCCCTCCACATTCTCAATTAAAGGTGAGCTAACGCCCTCGGTG
 TTTCTGATTAACAGTAAACCTAAATTCAAACCTGTTAATGACATTATTTATGTCTC
 TCTTAACATGAGACACATCTGTTACTGAATTCTTCAATATTCCAGGTGATAGATT
 TTGTCG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDA
WNFRPLDGGPEQFVFYHIDPFQPMSGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLFQHYRKKRWAER
AHKVVIEIKSKEEEERLNQEKKVSVYLEDTD

FIGURE 281

GCATTTGTCTGTGCTCCCTGATCTTCAGGTACCCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTGGGAGTTCCATCTTCTGGTCTGCCAGAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCAGCTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTACCAAATGGTTGGGATCTCCGAATGGTAGAGTGTGTCCTGGATGGAATCAGCTTGAGTCTCTGCAATTGGTCACAACATTCTAGCTTCTGTGATTTC
ATCCAACTAACCTACCTGCCTACGATATCCCCTTATCTCTAATCAGTTATTCTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAA

FIGURE 282

MKF~~L~~AVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTTAT
TAASTTARKDIPVLPKWVGDLPNGRVCP

FIGURE 283

GAGACTCTGAAGGTCCAAAGCAGCTGCTGAGGCCCAAGGAAGTGGTCAACCTTGGACCC
CTAGGGGCTGGATTGCTGGTTAACAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**
TACCTCCCTGCCCTTCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCTTGCGGAGAGA
GTGTCTGGTCAGGACGCAGAGGACGCTCACAGACTCCAGCCCTTGTACCGAGAGGAC
ACTTGGCAAGTCCAGCGATGGTCCGGAGTCCACACAGACTGGCGCAGGGCAGGAGGGG
GACAGTTCTGTGCTGGTGGACAGTAAGAGGGTCTGGCCAGTCCAGGGTGGGGGCG
GCAAACCTCCATAAGAACAGAGGGCTGGGCCACAGACTCATCTGCCAGCTCT
CTGCTGCTGCCAGTGGAGTGGCACAGGTGGGGCTTG GCCAG**TAA** AACACAGGCTGG
ATTGCGCTGCCAGTGGAGTGGCACAGGTGGGGCTTG GCCAG**TAA** AACACAGGCTGG
CCCCAAAGAGCTTCATTGTATATTGATTTTACACATTAGCAATTAAACTGAGAAAT
GGGCCGGCACGGTGGCTACGCCGTAAATCCAGCACTTGGGAGGCCAGGGCGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGGCTGCCAACATGGTGAACACTTGTCTACTAAAAA
TACAAAAAAATTAGCCAGGCACAGTGGTGTGCAGTGGTAGTCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGGCGACGGTGGCGTGAAGCCAGATCGGCCGCTGAT
TCCAGCCTGGCGACAAGAGTGAAGACTTCACTCACACA

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284/330

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWRDAEDAHRLQPFTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCCWPVGVARGGALCQ

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FIGURE 285

GTCA**TG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTACCCGGCCTGCCTCA
 GCGGCCCCCATGGCGGCCAGAACCTGGCACAGCATGAGGAGCTGACCTGCTTCCATGG
 GACCTGAGCTGGGCCAGGCCCTAACGGTGTACAGGACCACGGAGGGACGGCTGACAA
 AGGCCAGGAACGCTGGGTCTATGGCGACAATAGAACCTCTGGGCAGGAGGTGAGC
 CGGGGCCGGATGCAGCCCAGGAACCTGGCAACGCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGGCCACAGCTGAGGTGCTGGGGAGGTGGCCAGGCACAGA
 AGGTGCTACGGACAGCGTGCAGCGCTAGAACGCTGAGGAGCGCTGGCTGGCCCT
 GCCTACCGAGAATTGAGGTCTTAAGGCTCACGTCAGAACAGCAGGCCACATCCTATGGC
 CCTCACAGGCCACGTGCAGCGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTGCAC
 AGATCCAGGAGAGACTCCACACAGCGCGCTCCAGCC**TGA**ATCTGCCTGGATGGAACGTGAG
 GACCAATCATGCTGCAAGGAACACTTCCACGCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
 CCTGTTACTGGGATGCCAGGGCGCCGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGGGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGAGGGTGGAGGAAGGACATGTA
 CCCTTCATGCCACACACCCCTCATTAAGCAGACTGTCGGCATTTCAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELLLFHGTQLGQALNGVYRTTEGRLLTK
ARNSLGLYGRTIELLQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTGCCCGAGCCATGGCAAAGAATGGACTTGTAAATTGCAT
 CCTGGTGATCACCTTACTCCTGGACAGACCACAGGCCACACATCCAGATTAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAGTCATGCCCTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTACAAGAAATGCTACCTGCTCAGAAGGTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAGGAGGAATCCTGGTTATCCCAGGAACCTCGACGAAATCACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCGAGGTGTCATGACTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTGTTGACGTCAACGGAATCGTACATCCTCCCTCAACTGGG
 ACCGTGACAGCCTAACGGTGGCAAGCGAGAAAATGTGTCCTGTTCTCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTCGCAGCAGCAAGAGATAACATATGCGAGTTCACCATCCC
 TAAA**TAG**GTCTTCTCCAATGTCCTCCAAGCAAGATTCACTCATATACTTATAGGTTATGA
 TCTCTAACATCAAGTAAAATCATAAATTAACTTATTAAAAAAATTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTGCTAACACATTCTTGGGATTTGCCCT
 TCCTGGGGTATAGGGATCAGAAATATTGATCATGTCACGCGAGATAAAATGGCTTCTGCT
 AAACAGACTAAATCTTCTCTAGTCTTCTCACTGTACAAACCCAGTTGTTCTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAAGTTAGCGTATGTTGACTAACAAAATTCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAATTTCAGCCTGTCATCTGCTCCATGCTGGCAATAATACC
 TTGTCAGGCCATTACCTTATTTGAATTGCTCATCCTGTTGGGACTTGTATCTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTCTTCATGCC
 TACCTTTTTGGAAAGTTCCAGCGCAATTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTCATCCCCACCATGCTTACACCTCTAACTTAAATGGTAACCCCTAAGGCATAT
 CAAAGAAGCAGATTGCTGATAAACCGGAAATAGAAAAAAAGAACCTACATTATTTGCTT
 AGCATCCTACTCTCACCTTTATGAGATTGAGAGTGGACTTACATTCCCTTTTACATT
 TCGTATATTATTTTTAGCCATCATTATGTTAAAGTCTATTATGGCAACCAATCTT
 TGGAAGCTGAAAATGAAATTAAAGAATGCTATCTGGAAAATTGCTACGCTGTGCAATT
 TTTTATTCTGCCATTGCTTACAGTGTAACTGATTTAGGCTTAACTGACATTGACAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTAGACTTGGAGGGAAATGGCTTTTAGAAGCAAACAAATT
 AAATATATTGTTCTCAAATAAAATAGTGTAAACATTGAAATGTTGTTGAAACAATAT
 CCCACTTGCAAACTTAACTACACATGCTGGAAATTAGTTAGCTGTTTCAATTGCTCA
 ATAATAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMA KNGLVICILVITL LDQTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKH FHEANEDCISKG GILVI PRNSDEINALQ
DYGKRSLPVGNDFWLGIN DMVTEGKFVDVNGIAISFLNWDR AQPNGGKRENCVLF SQSAQGK
WSDEACRSSSKRYICEFTIPK

FIGURE 289

GCAGGGACCGGGTATAAGAACGCTCGTGGCCTTGGCGGGCAGCCGCAGGTTCCCCGCGC
CCCGAGCCCCCGCGCC**ATG**AAGCTGCCGCCCTCCTGGGCTCTCGGTGGCCCTGTCCCTGCA
GCTCCGCTGCTGCTTCTTAGTGGGCTGGCCAAGCCTGTGGCCAGCCTGTGCGCTG
GAGTCGGCGGCGGAGGCCGGGGGGACCCCTGGCCAACCCCTCGGCACCCCTCAACCGCT
GAAGCTCCTGCTGAGCAGCCTGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTGGC**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCCGAGGGCTGAAAACCCGCCGGGGAGGACCGTCCATCCCCCTCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAA
AAAAAAAAAAAA

290/330

FIGURE 290

MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVALESAAEAGAGTLANPLGTLNPLKLLLS
SLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTIVFG

FIGURE 291

TGAAGGACTTTCCAGGACCAAGGCCACACACTGGAAGTCTTCAGCTGAAGGGAGGCAC
 CCTTGGCCCTCGCAGCGATCAC**ATG**AAGGTGGCTGCCAAGTCTCTGCTCTCCCTCTGC
 GCACAGGTGCGCTGGTACCCGGCTGGCCCCCAGCTCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCGAGACCAGCAGGGTAGTCAGGCTCCAGGGAGGAAGAGGAAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAAAAGCTGGCTGATGCCAGGAGCAGCTT
 GCCAAGGAGACTCAAACCTCGGATTCAGCCTGTCGAAAGATCTCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCAGTCAGGGCTTAAGGCCACCAAG
 CCCGGCTCTGCCTTCCCTTAAGGACTCAGAGAGACCTCTCCCGAACCTGGAACT
 GGGCCTCTCACAGGGAGTTTGCCTTCATCCACAAGGATTTGATGTCAAAGGAGACTTCT
 TCAATTATCAAAGAGGTATTTGATACAGAGTGGCTGCTGATGAAATTTCGCAATGCCCTCA
 CAGGCCAAAGGCTCATGATATTACATAAAACAGAGACTGGGGAAAATTCCCAAAC
 GTTGATGAGATTAATCCTGAAACCAAAATTAAATTCTGTGATGATCTTGTCAAAGGGA
 AATGGTGAACCCATTGACCTGCTTCACCGAAGTCGACACTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCATGATGTACGGTGAGGCAAGTTGCTCCACCTTGTACAAGAGA
 TTTCTGGTGTATGCTCTCAAACCTGCCCTAACAGGAATGCCACATGCTGGTGTCTCA
 TGAGGAAAATGGGTGACCACCTGCCCTGAAAGACTACCTGACACAGACTGGTGAGACA
 TGCTCGAAACATGGGAGAGGAGAACATGGAAACTTTCTTCCAGGTTCAAGCTAGATCA
 GAAGATGAGATGATGAGCTGAGCTGCTTGGAGATGGAACTCAGAAGATCTCACCCTTG
 CTGACCTTAGTGAACTCTAGCTACTGGAAGAAATCTCAAGTATCCAGGGTTTACGAAGA
 ACAGTGAATTGAGGTGATGAAAGGGCACTGAGGGAGGCAAGTCTGTGAGAAATTAC
 TGCTTATTCCATGCCCTGTGATCAAAGTGGACGCCATTCTATTGATGATCTATGAG
 AAACCTCTGGAATGCTCTGTTCTGGCAGGGTGTGAATCGACTCTCT**TAA**ATTCA
 ACATGCTAAAGCACTCTGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACAGGA
 TACCGCAATGGATGGCAGGGAGAGGTGTTCTTGTCTTAACTAGTTAGGGTGTCTC
 AAATAAAATACAGTAGCTCCCACTTATCTGAGGGGATACATCAGAACCCCCCAGATGC
 CTGAAACGGTGGACAGTGCTGAACCTTATATATTCTACACATACACATACCTATGAT
 AAAGTTAATTATAAATTAGGCACAGTAAGAGATTAACAAATAACAAACATTAGTAAAAA
 TGACTTACTGAAACGCAAGCACTGCAATTACATACAGTCAGACTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGCGAGGAGCATAGACAGTGAGGACATTGGCAAGGGAGAAATCA
 CATCCTGGGTGGACAGCAGGAGCAGGAGCATGCAAGATCCACTCCACTCTGAGATGGCAGTC
 TGCTTAAGACTTTAGATTGTTATTCTGGAATTTCATTTAATGTTTGACCATGGT
 TGACCATGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAA
 GCATTAATTGATACATATTAAAAA

+ 4252660

FIGURE 292

MKVVPSSLLSVLLAQVWLVPGLAPSQSPETPAPQNQTSRVVQA
PREEEDEQEASEEKAGE
EEKAWLMASRQQLAKETSNFGBSLLRKISMRRHDGNMVFSPFGMSLAMTGLMLGATGPTETQI
KRGLHLQALKPTKPGILLPSLFKGRLRETLSRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYF
DTECVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKLILVDYILFKGKWLT
VFTEVDTFHLDKYKTICKVPMMYGAGKFASFTDKNFRCHVLKLPYQGNATMLVVLMEKMGDH
ALEDYLTTLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRI
FSPFADLSELSA
TGRNLQVSRLVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIYEETSGMLLF
LGRVVNPPLL

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCCGGACCCAGAC **ATGAG**
 GAGGCTCCTCCTGGTCAACCAGCCTGGTGGTTGTGCTGCTGGGAGGCAGGTGCAGTCCCAG
 CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
 GCCTGGGCGCCCGTGTGGTGAGCCTCCGGAGAAAGGACGACCAGCTGGTGGTGCTGTTCCC
 TGTCCAGAACGCCAAACTCTTGACCACCGAGGAGAACGCCACGAGGTCAAGGCAGGGCCCCA
 TCCTTCAGGCACCAAGGCCCTGGATGGAGACCGAGGACACCTGGCCGTGTCCTGAGTCCC
 GAGCCCGACCATGACAGCCTGTACCACCCCTCCGCCGTGAGGAGGACCAGGGCGAGGAGGCC
 CCGGTTGTGGGTGATGCCAAATCACCAAGGTGCTCTGGGACCGAGGAAGACCAAGACCACA
 TCTACCACCCCCAG**TAG**GGCTCCAGGGCCATCACTGCCCGCCCTGTCCCAAGGCCAGG
 CTGTTGGGACTGGGACCCCTCCCTACCCGCCAGCTAGACAAATAACCCCAGCAGGCAAA
 AAAAAAAAAAAAAAAA

0902521-114101

FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKA
WGVVEPPEKDDQLVVL
FPVQKPPLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHP
PPEEQGEE
RPRLWVMPNHQVILLGPEEQDQDHIVHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGTGAAGGAGCTCTG
 TACCCAAGGAAAGTGAGCTGAGACTCAGACAAGATTACA**ATG**AACCAACTCAGCTTCCTGC
 TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTCGTCTCCATCTCTGCCAGAACGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCATTGATGGCTGTATTTCTCCGCACTGAGAATGGTTATCTACCAAGACCTTCT
 GTGACATGACCTCTGGGGTGGCGCTGGACCCCTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGAGCGCAACTGGCCAACATACAACACCTTGGATTCAGAGGCGGCCAGGAGC
 ATGACTACAAGAACCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCCTCCAGACACTGGGACATAATCTGTTGGCATCTACAGAAATATCAGTGAAT
 ATGGAGAGGAAACTGTTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTGGC
 GACGCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGGGAAATTCACTGCGGGATT
 TGTTCAAGTTCAGGGTTAAATAACGAGAGAGCAGCCAACGCCCTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGGGAGGAGATACTTCCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTCTGGTTTGATGGAGTGGATATGAACTCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGT**TGA**GAGTTTG
 GGAGGGAAACCCAGACCTCTCCCAACCATGAGATCCAAAGGATGGAGAACAACTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAA

FIGURE 296

MNQLSFLLFLIAATRGWSTDEANTYFKEWTCSSSPLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGWTLVASVHENMDMRGKCTVGDRWSSQQGSKADYPEGDGNWANNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNPKSPMQHWNRNSLLRYRTDTGFLQTGLHNLFGI
YQKYPVKYGEKGKWTDNGPVIPVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEEHHCIGGGGYFPEASPOOCGDFSGFDWSGYGTHVGYSSEITEAAVLL
FYR

FIGURE 297

GCGGAGCCGGGCCGGCTGCGCAGAGGGAGCCGCTCGCCGCCACCTCGGCTGGAGCC
 CACGAGGCCTGCCGATCCCTGCCCTCGGAACAATGGACTCGGCGCGAGGTGCTTGGGCC
 CGCTGCTCTGGGACGCTGCAGGTGCTAGCGCTGCTGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGCATCTGCAAACATAGAGAAATTCTGGCTTCCACACAACACTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCTTCTGACCATAAAATGAAACTTCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCTCAGACTCCAGTAATAACACGGTCACCAACCATGAAACCTACAGCG
 GCATCTAATAACAACACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCACATCCACAATGACCG
 TAACCCACAATAGTTCACTGACATCTGCTGCTTCATCAGTAACAACTCACAAACAATATGCAT
 TCTGAAGCAAAGAAAGGATCAAATTTGATACTGGGAGCTTGTGGTGGTATTGTATTAAAC
 GCTGGGAGTTTATCTATTCTTACATTGGATGCAAATGTATTACTCAAGAAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAAATTGGTTTATTAAATAGTTAAACAAATATTCT
 CTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTCTCAAGGTAAACAGGGTTGGGTTTGAATAAACATCTGGATCTTATAGACCGT
 TCATACAAATGGTTTAGCAAGTCATAGTAAGACAAACAAGTCTATCTTTTTGGCT
 GGGGTGGGGCATTGGTCACATATGACCAAGTAATTGAAAGACGTCTACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTGTACAGCACTCAGGATTGGTATCTTTGTTG
 AGCTCACATAAGAACATTCACTGCTTTCAGAGCTGGATATCTTAATTACTAATGCCACA
 CAGAAATTATACAACTCAAACATAGATCTGAAGCATAATTAAAGAAAAACATCAACATTGGT
 TGCTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTIQLVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTMKPTAASNTTPGMVSTNMSTTTLKSTPKTTSVSQN
TSQISTSTMVTNHSSVTSAASSVTITTMHSEAKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAAII

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCCTGAGCCTGAGCCTGAGCCCAGCCCCGGAGCCGG
 TCGCGGGGGCTCCGGCTGTGGGACCGCTGGGCCCCAGCG**ATG**GCGACCCCTGTGGGAGGC
 CTTCTCGGCTTGGCTCTTGCTCAGCCTGTCGTGCCCTGGCGCTTCCGTGCTGCTGCC
 GCAGCTGTCAGACGCCAAGAATTTCGAGGATGTCAGATGAAATGTATCTGCCCTCC
 ATAAAGAAAATTCTGGCATTTATAAAGAACATATCTCAGAAAGATTGTGATTGCC
 CATGTTGTGGAGCCCATGCCCTGTGCCGGGGCTGATGAGAAGCATACTGTACGCTGT
 ATGCAAATATGAAGAAAAGCTCTGTACAATCAAGGTTACCATTTATAATTCTCTCCA
 TTTTGGGCCTTCTACTCTGTACATGGTATATCTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTTTGGACATGCACAGTTGATACAGAGTGTGATGATATTGGGATCACAGCCTT
 TGCAATGACACGATGTGCTAGCCCGCTCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACACGAGCGCTGGAAGCTCAAGTCCAAGGAGCAGCAGAAAGTGTCTTGA
 CATGTTGTCCTCAGC**TAA**TTGGAAATTGAATTCAAGGTGACTAGAAAGAACAGGCAGACAA
 CTGGAAAGAACTGACTGGTTTGCTGGGTTCATTTAATACCTGTTGATTCAACACT
 GTTGCTGGAAGATTCAAAACTGGAAGCAAAACCTGCTGATTGTTCTGTTAACGTA
 ATAATAGAGACATTTAAAAGCACACAGCTCAAAGTCAAGGAACTTCTATTG
 TGACTTTACTAATAAAAATAATCGCCGTAAATTATCTGAAGTCCTTACCTGGAACA
 AGCACCTCTTTTACACACATGTTAACCTGACTTCAAAGATAATTTCAAGGTTTTG
 TTGTTGTTGTTTTGTTGTTGTGTTGTTGCTGGGGAGGGGAGGGGATGCCCTGGAAAGTGGT
 AACAACTTTTCAAGTCAACTTAAACAAACTTTGTAATAGACCTTACCTCTATTG
 TCGAGTTCAATTATTTGCACTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGCTGCACCTCATGGTAAACGGGAT
 CTAAAATGCCGGTGGCTTCAAAAAAGCAGATTCTTCACTGTGACTGTGATGTCTGATG
 CAATGCATCCTAGAACAAACTGCCATTGCTAGTTACTCTAAAGACTAAACATAGCTT
 GTGTGTTGGTCTTACTCATCTCTAGTACCTTAAGGACAAATCTAAGGACTGGACACT
 TGCAATAAAAGAAATTTTAATTTAACCCAAAGCCTCCCTGGATTGATAATATACATTTG
 TCAGCATTCCGGTGGTGGTGGAGAGGGCAGCTGTTGAGCTCCAATATGTGCA
 AGGGCTGGGGTTGTGGTGCCTTCTGAAAGGTCAACCATTATTGATAACTGGCTTTT
 TCTTCTATGTCCTTTGGAATGTAACAATAAAATAATTGGATAACTGGCTTTT

12526650

FIGURE 300

MATLWGGLLRGSLLSCLALSVLLAQLSDAAKNFEDVRCKCICPPYKENSGHIYNKNIS
QKDCCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIYLSILGLLLLYMVYLT
VEPILKRRRLFGHAQLIQSDDDIGDHQPFANAHDLRSRSRANVLNKVEYAQQRWKLQVQE
RKSVFDRHVVLS

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTGGCTCTGTCGCTGCTGCCAAGGCCTCCTGCCCCGGGAAGCGG
CAGGAGCCGCCGACACCTGAAGGAAATTGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTCCAGAGGTCTCACCTGCCGAGG
CATTGCAAAGGCCAAGGATCAGGTGGAGGTGCTGGAGGGAGGTAGTGGAAAGAGGTCTG
ATGGGGCAGATTATTCAATCTACGGTTTGGGATTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAACATCTAACATATTACATTGAAAATCTAATATGGCGATAAAAA
TCATTGCTCACATTAAAATCTTATAGTCATAAAATTATTCAAATCCATCATCTCTTA
AATCCTGCCCTCTTCATGAGGTACTTAGGATGCCATTATTCAGTTCACATAAGAATG
TTTACTCAATGTTAACGTGTTTGCCTTAAATTCAACAACTAACAAGGCAGAACTAGGACTT
GAACATGGATCTTGTTCTTAATCCAGTGAGTGATAACATTCAATGCACTCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPAFLSRGKRQEPPPTPEGKILGRFPPMMHHHQAPS
PGARFQRSHLAEAFAKGSGGAGGGSGRGLMGQIPIYGFIFLYILYILFKVSRIILI
ILHQ

FIGURE 303

CGGGCTGAGTGCAGCTGTGGGGAGATTCACTGCATTGCCCTCCCTGGGTGCTTTCATCTT
 GGATTTGAAAGTTGAGAGCAGC**ATG**TTTGCCCACGTAAACTCATCCTGCTGCCAGTGTAC
 TGGATTATTCCCTGGGCTGAATGACTTGAATGTTCCCCGCTGAGCTAACAGTCATGTG
 GGTGATTCAGCTCTGATGGGATGTTTCAGAGCACAGAACAAATGTATATTCAAGAT
 AGACTGGACTCTGTCACCAGGAGACGCCAGCAAGGAGCAATATGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGCGCTTCCAGAACCGCTACACTTGATGGGGACATCTTATGC
 AATGATGGCTCTCTGCTCCAAGATGTCAGAAGAGGCTGACCAGGGAAACCTATATCTGTGA
 AATCCGCTCAAAGGGAGAGCCAGGTGTTCAAGAACGGCGGTGACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTATGGTCCATGTGGGTGGATTGATTCAGATGGGATGTTTCCAG
 AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTCAAGGACGGCGCGCAAAGGA
 GGAGATGTTATTCGTTACTACCACAAACTCAGGATGTCGTGGAGTACTCCCAGAGCTGGG
 GCCACTCCAGAATCGTGTGAACTGGTGGGGACATTTCCGCAATGACGGTTCATCATG
 CTTCAAGGAGTGAGGAGTCAGATGGGAAACTACACCTGCAGTATCCACCTAGGGAAACCT
 GGTGTTCAAGAAAACATTGTGCTGCATGTGACGCCGAAGAGCCTCGAACACTGGTGA
 CGGCAGCCCTGAGGCCCTGGCTTGGTGGTAATCAGTTGGTGTGATATTGGGAAATTGTC
 TGTGCCACAATCTGCTGCTCCCTGTTCTGATATTGATCGTAAGAACGACTGTGAAATAA
 GAGTTCACTGAAATTCTACAGTCTGGTGAAGAACAGAAGAACAGACTAATCCAGAGATAAAAG
 AAAAACCTGCCATTGGAAAGATGTGAAGGGAGAACACATTACTCCCCATAATTGTA
 CGGGAGGTGATCGAGGAAGAACCAACTGAAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTGGCTTCTGAGGTCAAGATCGAACACTCACTGAAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTT**TGA**GAAGAACGAGTCCCTCATCTCAGCAGCGG
 TGGAGACTCTCCTGTTGTCCTGGGCACTCTACAGTGTGATTCAGACTCCGCTCTC
 CCAGCTGCTCCTGTCATTGTTGGTCAATACACTGAAGATGGAGAACCTGGGCGT
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCGCTGCTGAGGGGGAGGAGCATGGACTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTTGGCCTAAACCCCCCGTT
 GGATCAGACCCCTCCTGGGAGGGTCTTAGTGGATGAGTTACTGGGAAGAACAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLSPE
EHAKDEYVLYYSNLSVPIGRFQNVRHLMGDLCLCNDGSLLLQDVQEADQGTYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHGGLIQMGCVFQSTEVKHVTKEWIFSGRRAKEEIVFRYY
HKLRLRMSVEYSQSWSGHFQNRVNLVGDIFRNDGSIMLQGVRESDGNNYTCIHLGNLVFKKTIV
LHVSPEEPRTLVTPAALRPLVLGGQNOLVIIIVGIVCATILLLPVLILIVKKTGNKSSVNSTV
LVKNTKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNNSLEKKSGGGMPKTQOAF

FIGURE 305

CTATGAAGAACCTCTGGAAAACAATAAGCAAAGGAAAACAATGTGTCCCACATG
 GTTCTACCCACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
 AAACTACATTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAAGCC**ATGCA**
 GGATGAAGATGGATACATCACCTAAATATTAAAACCTGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTGGTGGCGTGTGATGGCTTGATTCTGCTGATCCTGCGTGGGG
 ATGGTTGTCGGGCTGGCTCTGGGATTGGCTGTGATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGCAATATGTGG
 TAAAACAATCAGAACTAAAGGGCATTCAAAGGTCAAAATGCAAGCCCCGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTCTTCAGGCACAACTAACATGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTAATTGTTGGTCGGATTATCTGCCAGAAGTCGAAT
 GAGGCTGGAAGTGGAGGATGGCTCGGTTATCTCAGAAAATATGTTGAGTTTTGGAAGA
 TGGAAAAGGAAATATGAATTGTCATTTCATAATGGAAAATGCACCTACCTCTGTG
 AGAACAAACATTATTAATGTTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTATTGTACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAA

FIGURE 306

MQDEDGYITLNKTRKPALSVGPASSSWRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHILRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVQDQLP

FIGURE 307

CCCACCGCTCCGCGCAGTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCC CGA TCCC GG
 CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGC GCGGGAGCCGGACC G C
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCTTGCTGAAGCCC GAGTGC GGAGAA
 GCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGGAGGGAGGGCAACCCAGAGAGGGG CAGCAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCCATGGCGCGCTATGCCAGCTCGCTATCGTCAGAAAGAGGCAAGCCCGC
 AGCGCGAGAAATCCAAGCCTGCAAGTGTGTCAGCAGCCCGCAGCAAAGGCAAGACCAGCTG
 GACAAAAACAAGTTAAATGTTCTTCCC GG GTCAAACCTCTCGGTCCAAGAAGAGGCGC
 AAGAAGACCAAGAGCCTCAGCTTAAGGGTATA GTTACAAAGCTATACAGCCGACAAGGCTAC
 ACTTGCA GCTGCA GGGGATGGA ACCATTGATGGCACCAAGATGAGGACAGC ACTTACACT
 CTGTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGTAACTTGTA CACCTCGGAACTTTCACACTGAGTG
 AATTCAAAGAATCAGTGTGTTGAAAATTATTATGTGACATATTCAATCAATGATATAACCGTCAG
 CAGCAGTCAGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAAGCCTGCAGCTCATTTCTGCCTAAACCAACTGAAAGTGGCATG
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCGATCTGGAAGGGGACCCAAAC
 AAGAGCAGAAGTGTCTCTGGCGTGTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
 GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTACCCAAAAGTTCAAATTGTGACATTACCAAAACAAACAGG
 CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREEREKSACKCVSSPSKGKTSCKNKLNVFSRVKLFGSKKRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGKTDESTYTLFNLIPVGLRVVAIQGVQTKLyla
MNSEGYLYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGHNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSRGSGPTKSRVSGVLNGGKSMSHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGCCTGTATGCCATATTATTGTTCTATGCTACTAGACATGGGGGG
 ACTTGGTGA~~AAA~~AGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTGGGGGATTCAGTGAAAAAAGTGGGGATCCCCT
 CCATTTAGGTAGCAAAGGAAAAAACCCAAGGTTGGGTCCTCTGACATTGGCAGTG
 CCCAGTAGGGTGGGATGAGCGAATATTCCAAAGCTAAAGTCCACACCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCCAAATACAGTGGAAAGGTGCCTGAAGATATTAA
 ACCACGTCTGGAAATTAGTGGGTCTGGCTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGAAAGGGGACGTTTCAATAGGAGGAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGTA~~ACTGGCTGCT~~
 GTGGAGGGGGTACGTGAGGGGGGGTCTGGGCTTACCTCAGGTCTGTGGGTGGGCGAG
 CGAGTCGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGAGGCCAG
 CGCGCTCGGGCGCCTGCCGGTTGGGGTGTCTCTCCGGGGCGCTATGGCCGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGAGGTCCGCCAGGCCGGGGCAGCCGGCCGGTGTGG
 CGCAGCGGCGCGTGTCTCCCGCCGACCAAGTCCCTTGCCAGAAGCAGCTCCATCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGCGGCCGCGCCGGACCGCGGCCGGAGCCTCA
 GCTCAAAGGCACTGTCACCAAACGTTCCTGCCAGGGTTCTACCTCCAGGGCAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCTCACCCACTCAACTGATCCCT
 GTGGGCCTCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGATTCACAGCTGAGTGTGCTTAAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCCTCTGCTCTACCGCCAGCGTGTCTGCCGGGCC
 TGGTACCTCGGCCTGACAAGGAGGGCCAGGTCA~~G~~AAGGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCACTTCTGCCAAGCTCTGGAGGTGGCCATGTACCAGGAGCCTCTC
 ACAGTGTCCCCGAGGCTCCCTCAGTCCCCCTGCCTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCAACCTGT

FIGURE 310

MAALASSLIRQKREVREPAGGSRPVSAQRRCPRGTTKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTAAAHFLPKLLEVAMYQEPLSHSVPEASPSSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATG GCGCGGGCCATCGCTAGCGGCTTGATCGGCCAGAACGGCAGGGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACCG
GCAACCTGGTGGATATCTTCTCAAAGTGCATCTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCAGCTAAGGGTATAGTGACCAGGTTATATTGCAAGGCAAGGCTACTACTT
GCAAATGCACCCGATGGAGCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTCATCCAGGGAGTGAAAACAGGGTTGAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTGAAGGTTATGTAATCTACTCATCCATGTTGACAGACAACAGG
AATCTGGTAGAGCCTGGTTGGGATTAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCGCAGCTCATTTCTACCCAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTGCATGATGTTGGGAAACGGTCCCGAAGCCTGGGTGACGCCAAGTAAAA
GCACAAAGTGCCTGCAATAATGAATGGAGGCAACCAAGTCAAAAGAGTAAGACAACTAG

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
><subunit 1 of 1, 247 aa, 1 stop
><MW: 27702, pI: 10.36, NX(S/T): 2
MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYYLQMHPDGALDGTKDSTNSTLFNLIIPVGLRVVAIQGVKTGLY
IAMNGEKYLYPSELFPECKFKESVFENYYVIYSSMLYRQQESGRAWFGLLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSKT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAAT
 GAAGGATGCAGGACGCAGCTTCCTGGAACCGAACGCAATGGATAACTGATTGCAAGAGAGAGAAAAGA
 ACGAACGCTTTCTTGAGCCCTGGATCTAACACRAATGTATATGTGCAACAGGGAGCATTCAGAAATG
 AAATAAACAGAGTAGACCCCGGGGGTTGGTGTCTGACATAATAATCTAAAGCAGCTGTCCC
 CTCCCCACCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATCACAAAGAAAAAGTATGTTATT
 TTCTCTATAAAAGGAGAAAGTGACCAAGGAGATAATTGGAAATGAAAAGTTGGCTTTTAGTAAAGTAA
 AGAACTGGTGTGGTGTCTTCTTCTTTGAATTTCACAAGGAGAGGAAATTAAATAACATCTGC
 AAAGAAATTTCAGAGAAAAGTGACCCGGCAGATTGAGGCACTGATTGGGGAGAGAAACCAGCAGAGCA
 CAGTTGGATTGTGCTATGGTACATAAATGGCAGGATAATTGAGTGGGGTTCTCATACCTCCCTT
 TTTAAATTATTCTTCTTGGTATCAAATCATGCTTCTCTGTCTTAACCCATGGATTCTACATCT
 GGATGTTGCTGTGATCAGTCTGAATAACACTGTTGAATTCCAGAAGGCCAACACCCAGATAATTATGA**ATG**
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTTAGGTTAACAGGGCCATTGGACCCCT
 GCTTGTGGTGTGCTGGCTCTCAACTCTGTGGTGGCTGGTGTGGCGGGCTCAGACTGCCCTCTGTG
 GCTCTGCAAGCAACCAGTTCAGCAAGGTGATTGTGTTGGAAAAACCTCGCTGAGGTTCCGGATGGCATCTC
 ACCAACACACGGCTGCTGAACCTCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAG
 GCACITGGAAATCCACAGTTGAGTAGGAAACCATATCAGAACCAATTGAAATTGGGGCTTCTCAATGGTCTGGCA
 ACCTCAACACTCTGGAACACTTGTGCAACATGGCTTACTACATCCCGAATGGAGCTTTGTATACTTGTCTAA
 CTGAGGGAGCTGTGGTGGAAACACCCATTGAAAGCATTCTTATGCTTTAACGAAATTCTTCTT
 GCGCCGACTAGACTAGGGAAATTGAAAAGACTTCAATCATCTCAGAAGGTTGCCATTGAAGGTCTGCCACT
 TGAGGTTATTGAACCTGGCATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAG
 CTGGATCTTCTGGGARATCATTATCTGCCATCAGGCCCTGGCTCTTCAGGGTTGATGCACCTCAAAACCT
 GTGGATGATACAGTCCCAGATTCAAGTGTGAACGGAAATGCCCTAGTCACTAGTGGAGATCA
 ACCTGGCACACAAATACTAACATCTGCTCATGACCTCTTCACTCCCTGATCATCTAGAGCGGATACAT
 TTACATCACACCCATTGAACTGTAACTGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCTC
 GAACACAGCTTGTGTCGGGTGTAAACACTCTTCCCAACTAAAGGGGAGGTACATTGGAGAGCTGCCAGA
 ATTACTTCACATGCTATGTCGGGTGATTGGAGCCCCCTGAGACCTCAATGTCAGTCAAGGGCATGGCAGT
 GAGCTGAATGTGGCCCTCACATCTGACATCTGTATCTGGATTACTCCAATGAAACAGTCACTGACACA
 TGGGGGTACAAAGTGGGATGACTGTGCTCAGTGTGGTACGTTAAATTCCAAATGTAACGTGCAAGATA
 CAGGCATGACACATGTGGTGGTAATTGGTGGGAAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCA
 GCAACCAACTACTCTTCTTCAACTCCAGTCAGTAGAGACTATGAAACCGCTCAGGATGAGGACAG
 GACCACAGATAACAAATGTGGTCCACTCCAGTGGTGACTGGAGACCACCAATGTGACCACCTCTCACAC
 CACAGAGCACAAGGTCGACAGAGAAAACCTTACCATCCAGTGACTIONTAAACAGTGGATCCAGGAATT
 GATGAGGTGATGAAGACTACCAAATCATCATGGGTGTTTGTGGCCATCACACTCATGGCTCAGTGTGCT
 GGTCTATTCTACAAAGATGAGGAAGCAGCAGCATGCCAAACCATCAGGCCAACACAAGGACTGTGAAATT
 TTAATGGGATGATGGGATGAGGATGGGGAGACACCCATGGAAAGCCACCTGGCTCATGCTGCTATGAG
 CACCTAAATCACTATAACATCACAAATCTCCCTCAACCCACAAACAGTTAACACAAATAATTCAATACA
 CAGTTCACTGATGAACCGTTATTGATCGGAATGACTCTAACAGAACATGTACAAGAGACTCAAAT**TAAAC**
 TTACAGAGTTACAAAAACAAACATCRAAAAAAGACAGTTTAAAGACACAAATGACTGGGCTAA
 ATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAAATTATTATTAACCTATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRALFDPLLVLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLKEWLRLNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAEFEGLSNLRYLNLMCNLRIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHHNLTLLPHDLFTPLHHLERIHLHHNPWNCNCIL
 WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGEELDQNFTCYAPVIVEPPADLNVTGMAAE
 LKCRASTSLTSVSWITPNGTMTHGAYKVRIAVLSDGTLNFTNVQDTGMYTCMVSNSVGN
 TTASATLNVTAATTFFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
 HHAPTRTVEIINVDDETGDTPMESHLPMPAIEHEHNLHYNSYKSPFHHTTVNTINSIHSS
 VHEPLLIRMSKDNVQETOI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCCTGCCCCAGGGGCACGGGGCGGGGCCGCTCCGCCGGCACAT
 GGCTCAGGCCACCTCGCGCACCCGAGGCAGCGCCAGCTGCCAGGTCCGTCGGA
 GCGCCGGCGCCGCCGGAGCCAAGCAGCAACTGAGCAGGGAAAGCAGCCCGTCCGGGATC
GGGATGTCCCTCTCCCTCTCTCTGCTAGTTCTACTATGTTGAAACCTTGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGAAAAGGTCACTTGCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTCACCGATAATGAAGGGAAACCAAAA
 GTGGTGATCACTTACTCCAGTCGTCATGTCATAACTTGAAGTGTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTGCTCCAAATTCTCGAGGAGATGCTCCCTGCAAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCGGTACACCTGTAAGGTTAAAGATTCAAGGGCGTACGTGTGGAGCCAT
 GTCATCTAAAAGTCTAGTGAGACATCCAAGGCCAAGTGTGAGTTGAAAGGAGACTGAC
 AGAAGGAAGTGGCTGACTTGTGAGTCATCTGCCACAGAGGCCATTGTGATT
 ACTGGCAGGAATCGAGAGAAAAGAGGGAGAGGTGAACGTCGCCAAATCTAGGATT
 GACTACACCAACCTGGAGAGTTCTGAGAATCTTACATGTCCTACTCTGGACTGTA
 CCAGTGACAGCAGGCCAACAGTGGAGAAGGAAAGCTGTGTCGCAACTGTCAGACT
 ATGTACAAAGCATCGGCGATGGTGCAGGAGCAGTGACAGGCAATGTGGCTGGAGCCCTGCTG
 ATTTCCTCTGGTGGCTGAATCCGAAGGAAAGACAAGAAAAGATATGAGGAAGAAGA
 GAGACCTAATGAATTGAGAAGATGCTGAAGCTCCAAAAGCCGCTTGTGAAACCCAGCT
 CCTCTCTCGAGGCTCGGAGCTCACCTCTGGTCTCTGCTCCACTGCTCCACACAAAAT
 AGTGGCTCACGCAGGCCAGCGGACACTGTCACTGTGACCCAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCTAGTGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
 CTAATCTGACCAAAGCAGAACCCACCCAGCATGATCCCGACCCAGAGGAGCCCTTCAA
 ACGGTCTGAATTACATGGACTTGACTCCACGCTTCTAGGAGTCAGGGCTTGTGACTC
 TTCTGTCATTGGAGCTCAAGTCACAGCACACACAGATGAGAGGTCACTAAGTAGCA
 GTGAGCATGACGGAACAGATTGAGCATTTCCTTACATAACAAACAAAGCAAAA
 AGGATGTAAGCTGATCATCTGAAAAGGCATCTTATTGTGCTTTAGACCGAGATAAGGG
 AAAGCAGGAGTCCAAATCTATTGTGTCAGGACGGCTGTGGTGAAGGTTGGGAAAGGTG
 AGGTGAATATACCTAAAATCTTAAATGTGGGATATTGTGATCATGCTTGTGATTCAAATT
 TTCAAGAGGAATGGATGCTGTTGAAATTCTATGCAACTTCTGCAAACACTATTGGATT
 ATTAGTTACAGACAGTCAGCAGGAAACCCACAGGCTTACACCTGTCAACCATGTAC
 TGAGCTAACCACTCTAAGAAACTCCAAAAGGAAACATGTGCTTCTATTCTGACTTAAC
 TTCATTGTCTAAGGTTGGATATAATTCAAGGGAGTTGAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTCTCCACACTATACATAACTATCTGCAACTATTGTGATTGAGCCAAAATAAC
 TATGAAAGGAGACAAAATTGTGACAACAGGATTGTGAAGAGCTTCCATTCATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTCCCTCAAAT
 CAGATGCCCTAAGGACTTCTGCTAGATATTCTGAAAGGAGAAAATACACATGTGATT
 TATCAACGCTTCTAGAAAAGAATTCTCTAGAGAAAAGGGATCTAGGAATGCTGAAAGGATTA
 CCCAACATACCACTTATAGTCTCTTCTGAGAAAATGTGAAACCAAGAATTGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTCTCTTAAATATGTCAGGAAGGTAGCCGGCA
 TTGTCAGGCCACCTGAGGAAAATCCAGCAGGTGGAGGTTGCAAGGACTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGTGCAGAGCGGGACTCCGTCTC

FIGURE 316

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41281, pI: 8.33, NX(S/T): 3
MSLLLLLVSYYVGTGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPCKELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLIRRKDKERYEEERPNEIREDAEAPKARLVKPSSSSGSRSSRGSSSTRSTANS
ASRSQRTLSTDAAQPGLATQAYSLVGPEVRGSEPKVHHANLTKAETTPSMIPSQSRAFQTV
```

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGGNGCGCGGGGAGCCCTGGGACCAGGAGCGRAGGCCGCCTACCTGCAGCCGCCGCCACGGCACGGCA
 CC**ATG**CGCCTCTGTGCTGCTCTGTGCGGAGTAGTGGATTTCGCCAGAAGTTGAGTATCAGTACT
 CCTGAAGAGATGATTGAAAAGGCGAAAGGGGAAACTGCCCTATCTGCCATCAGAATTTACCTTAACTGCTTAACTGCGGAAAGA
 CCAGGGACCGCTGGACATCGAGTGGCTGATATCACAGCTGATAATCAGAGGTGGATCAGTGATTATTTAT
 ATTCCTGGAGACAAATTTATGTGACTACTATCCAGATCTGAAAGGCCGAGTACATTTACGAGTAAATGATCTC
 AAATCTGGTGATGCATCAAATATGTAAACGAAATTCAACTGTGAGATATTGCCACATATCAGTGCAGAGTGA
 AAAAGCTCTGGTTGCAAAATAAGAAGATCATCTGGTAGTTAGGCTTAAAGCCTTCAGGTGCGAGATGTTACG
 TTGATGATCTGAAGAAAATTGGAAGTGACTTAAAGTGAACCAAAGAGGTTCACTTCCATTACAG
 TATGAGTGCACAAATTGTCTGACTCACAGAAATGCCAACCTCATGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTAAAAATGCTCTCTGAGTACTCTGGGACATACAGTGTACGTTAAAGCAGTGGCTCTGATC
 AGTGCTGTGCTTAACAGTGTGCTCTCTCAAAACAGTGTGACTATTGCAGGCCCATTAGAGAACT
 TTGCTGTCTAGCGCTCATGGCTTATCATCTTTGTGCTGCTAAAGGCCAGAGAAGAAAATATGAAA
 GGAAGTACATCAGGATATCAGGAAAGATGCCACATCAGGAAAGGCCGAGTACGTCACTGCCAGAGTACATCG
 GCAGTAATCATTCCTGGCTCATGTCTCTTCAACATGGAGATATTCCAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTGAACGCCACTCTCAGAGTCCGACTCTCCACCTGCTAAGTCAAGTACCCATACA
 GACTGATGGAATTACAGTGT**ATA**ATGAGACTCTGAGAATCTGAGATTTGATTATGACTTTT
 AGGCCTCTAGTAAAGACTTAAATGTTTAAAGCACAAGGCACAGAGTTAGAGCAGCTGTAAGRACAC
 ATCTACTTATGCAATGGCATTAGCATGTAAGTCAAGTGTCTGATGTTAAAGTGTGAAATTCTTGT
 TAAAACCCATGATAGTGAACCTGATGATGTTAAAGATGTTTATATATTCAATACACTAACAA
 ATTGAACTTCTTATCATGATATTCTGATGTTAGGTTAAAGTGTGTTAATGTTGATTITCA
 AGGAAATTTTAAAGTCTTACGTTCTGTTTGTCTATTAGTTAAATCATGAGGGAAATACCCG
 TTCTTCCCCTTATGCACACAAAGACAACCGCTTGTCTGCTCAAACACTTATTTATGCAACTACA
 TGATTGCAACAAATCTCTTAAAGCACACGATAAAATAGTCTCTGTATATAAATACCTACAGCTCCA
 TAAAGTAATCTCAAGGTGCTAGAACAACTGCTTCAACTCTGACTGTTCTGCTATCAAACAGAGTGTG
 ACAAAATTAATCTAACGCTTAAAGTCACTTAAAGTAACTTAAAGTCTGACTAACTTAAATTTCTCAACTA
 TATCAATCTAAAGTGTCAATTATTGAAAGATTCTCAACTTAACTCTATAAATGTTGATTG
 TTGCTCACATGACACCAACAACTCAAAAACGAGTTAGTGAGGCTAACATGTGAGGATTAACTCAGTGT
 TCCGGTCACATGCTTCCAGGGAGGGTACCCATGCTACTGAAATTGGGCGATATGGTTATTTCTCC
 TGATTGATAACCAATGGAAACAGGGAGGGAGGATGTGATTCTGATGGCATTCTCGATACATTCTGGCTT
 TTTCTGGGAAAGGGTGGCAATTGGGAAAGTGGAAATATAAGTCTGAAATCTGAGGGAAAGAACACAT
 TAAGTTAATCTCAAGGAAAATCATCATTAAGTCCAGATTCTCATTAAAGACAAAGTTACCCACACACT
 GAGATCACATCTAAGTGCACCTCTATGTGCTAGGTCTAAATCATTTAAACCTCATGTGAAATGGGTATAA
 TGTATAACAGGTGACCAATGTTTCTGAAATGCTAAAGAAATGAAACAAACTCAGTACTCTCAAAACAA
 CTTCACCAAAAAGACCAAAACATGGAAAGATGGAAAGCTTGTAGGACATGTTTACTGCTGTT
 CCACAGCTGCTAAGGGAGGTCACTTGGAGGCTTAAATACAAAATCTGGAGCTGGAGGCAATTATCCT
 ACCAAACATATGCGAAACAGAAAATCAACTACCGCATGTTCTCACTTAAAGTGGGAGGTAATGATAAGAAC
 TATGAAACAAAGAAAGGAAACATGACATTGGAGTTATGGAGGAGGGGGAGGAGGAGGAAAGGAGCA
 GAAAAGATAACTTATGGAGTACTGCCCTCACACCTGGGTGATGAAATAATGTACAACAAATCCTGTGACACA
 TGTTTACCTATGGACAAACCTTCATGTGATCCCTAACCTAAAGTTAAAAAAAARAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAARAAAAAAAARAAAAAAAARAAAAAAAARAAAAAAA
 AAAAAAAAAAAAAAAAARAAAAAAAARAAAAAAAARAAAAAAAARAAAAAAAARAAAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
><subunit 1 of 1, 352 aa, 1 stop
><MW: 38938, pI: 7.86, NX(S/T): 3
MALLLCFVLLCGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNNDLKGDAINVTLNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDQCLLRLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIIFCCRKKRREEKYEKEVHHDIREDVPFPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302**Myelin P0 protein.**

amino acids 96-125

404774 T2526660

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCACCCACAGCTATGCCCTGTATTGGTGA
 ATGGTGAAGGTGCCTGCTAACTTTCTGTAAAAAGAACCGAGCTGCCCTCAGGCAGCCAGCC
 CTCAACGATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTCGC
 CAATTAAACACCAAGAAGAATTGAGGCTGCTGGGAGGAAGGCCAGGAGGAACAGAGACTG
 AGAG**ATG**AATTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTGCCCTGGGTTTACCCCTG
 CTTCTCTGGAGGCCAGGTATCAGGGCCCAGGGCCAAGAACATCCACTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAAACTGTGGGAAGCCTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACAGGTGCCCGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCCTGCTGGAGTTCTACTTGAAAAGCTGTTTCAAAA
 CCACCCACAATAGAACAGTGAAGTCAGGACTCTGAAGTCATTCTACTCTGGCCAACAACT
 TTGTTCTCATCGTGTACAACGTCAACAGTCAGGAAATGAGATGTTTCCATCAGAGAC
 AGTGCACACAGCGGTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAACAGC
 TCTGACCAAAGCCCTGGGAAGTGGACATTCTCTGACCTGGATGCAAGAAATTCTACAAGC
 TC**TGA**ATGTCAGACCAAGGACCTCCCTCCCTGGCACTGGTTGTTCCCTGTCATTCA
 AACAGTCTCCCTTCTATGCTGTCACTGGACACTCAGGCCCTGGCATGGGCCATTCTC
 TTGGCCCAAGGATTATTGTCAAAGAACAGTCATTCTTAAGCAGGCCAGTGACAGTCAGGGAAAG
 GTGCCCTGCGATGCTGTGAAGAGTCACAGAGAACATTCTGTATTATTACAACCTATTT
 AATTAATGTCAGTATTCAACTGAAGTTCTATTATGTCAGAACAGTCAAGTTACATGAAGG
 CAGCAGAAATTGCCCCATGCTCTTACCCCTACAATCCTGCCACAGTGTTGGGCCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAAACTGTGGTGTCTGGCTGCTTGGCTGTCTGGATT
 GTAAAAAAACAGAGAGGGATGCTGGATGTAAACTGAACCTCAGAGCATGAAACACT
 GTCTCTGATATCTGCAGGGACAGAGCATTGGGTGGGGTAAGGTGCATCTGTTGAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCTGGAGCACAAGCAGTCCTCAATAAACATTCTC
 TCCCACCCACACTGCCAGCTCACCCCATCATTCCCTGGTGCCTCCCTTGGCTGCTTGGATT
 TATCCTAGTCATTCTCCCTAATCTCCACTTGAGTGTCAAGCTGACCTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAGACAACATAA
 CTCCAAAAA

320/330

FIGURE 320

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
><subunit 1 of 1, 206 aa, 1 stop
><MW: 23799, pI: 9.12, NX(S/T): 3
MNFQQRLQSLWTLARPFCPPLLATASQMQMVVLPCLGFTLLLWSQVSGAQGQEFGFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSADAESCYLVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSFLANNFVLIVSQLQPSQENEMFSIRDSAHRFFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL
```

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

ID: 320/330 = X252660

FIGURE 321

AAGGAGCCAGCCCCCAAGCACCAACTGAGAGGC**A**T**G**AAGTTACAGTGTGTTCCCTTGGCTC
CTGGGTACAATACTGATAATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAATGTCACTATCCTGCCAACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCTCTACGTGGACAGGGTGTCAAGGATCA
TCAGGAGCCAAACCCAAAATCTTGAGAAAATCAGCAGCATTGCCAACTCTTCCTCTACA
TGCAGAAAATCTGCCGAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGGCCACC
AATGCCACCAGAGTCATCCATGACAACATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGTATCCAGGGATGAACACCCCCCTGTGCGGTTTACT
GTGGGAGACAGCCCACCTGAAAGGGAGGGAGATGGGAAGGCCCTTGAGCTGAAAGTCC
CACTGGCTGGCTCAGGTGTCATTCCGCTTGAAGAAACTCTAAGCAGGCTGAGTGTGGTAT
TTGTAATAAAACTCTATCTGCTGAAAGGGCCTGCAGGCATCCTGGGAGTAAAGGGCTGCCCT
CCCATCTAATTATTGAAAGTCATATAGTCCATGTCAGTGTGAGCTGAGCCAAAGTGTATCT
GTAGTACACATTGTAAGTGAGTGGTTTCTGAATAATTCCATATTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHEESFQEIKRAIQAKDTFPNVTILST
LETLQIPIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQRQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

12526650

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCTATAGAGTCATAAGCCCCACTGGCTTCGTAG
AACGCGGCTACAATTAAATAACATAACCTTATGTATCATACACATACGATTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTCTCCACAGGTGTCACCTCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACAGCCACTCAGAGCAGGGCAGC**ATG**TTGGGGCCCGCCT
CAGGCTCTGGGCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCTATCCCA
ATGCCTCCCACTGCTCGCTCCAGCTGGGTGGCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAAATGCCATGTGGATGGCGACCCCATCAGAC
CATCTACAGTGCCTGATGATCAGATCAGAGGATGCTGGCTTGTTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTGGATCACACTATTCGAC
CCGGAGAACTGCAGGTTCAACACCCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
TCAGTATCACTTCTGGTCAGTCTGGCCGGCGAAGAGAGCCTCCGCCAGGCATGAACC
CACCCCCGTACTCCCAGTCCCTGTCGGAGAGAACGAGATCCCCCTAAITCACTTCAACACC
CCCATACCAACGGCGCACACCCGGAGCGCCGAGGAGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCGGATGACCCGGCCCGCCTGTTACAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGCCAGTGACCCATTAGGGTGGTCAGGGCGGTGAGTGAAC
ACGCACGCTGGGGAACGGGCCCGAAGGCTGCCGCCCTCGCCAAGTCATC**TAG**GGTCG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238
><subunit 1 of 1, 251 aa, 1 stop
><MW: 27954, pI: 9.22, NX(S/T): 1
MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGLIHLYTATARN SYHLQIHKGHVD
GAPHQT IYSALMIRSE DAGFVVITGVMSR RYLCMDFRGNIFGSHYFDPENCRFQHQTL ENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNVLKPRARMTPAPASC SQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

202526660

FIGURE 325

GGAAAAGGTACCCGGCAGAGACAGCCAGCAGTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTGGGGCTGGCTCTGCCCTTTCTTCTCTGTGGAGGTTGGGGCTCTGG
 GAGCTCTGCAGGGCCCAGCACCCGAGACAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCACGCCAGCTGGAACTCAAACGCTGAGCCTGAG
 ACCTCTCTAGGGCTCAACCCCAGCCGGCCCATTCCAGAACGAGACCAGGGAGCCAA
 GAGAATTCCCCCTGCAAGAGAGACCAAGGAGTTCAAAAAACATCTCCAACCTCATGGTGC
 TGATGCCACCTCCGGAGACATCAGCGCCAGTGGCAGGCCAGGGAGCTGGAATGACC
 ACAGTTCAAGACCATCACAGGCAGTGATCCCAGGAAGGCCATTTGACACCCTTGACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAACGTAAGGGCTGTCTCAGAGAGCAGTGCTCTTCGACGCCCATCCAGTCATC
 ACCCGTCACGGCCTCAGAGAGCAGGCCCTTCGACGCCCATCCAGTCATC
 GTCACGGCCTCAGAGAGCAGGCCCTTCGACGCCCATCCAGTCATC
 GGTCCCCGGGATCTGATGCACTCTCTCGCTGAAGGCTGGTACTGTCACAAACATCGAG
 GTTATTAAATTGCAAGCATCACAGAAAATAGAAACAACAACTTCAGCATTGGCTCAGA
 CATAGATCTCATCCCCAGGAAGGGGTGAAGGCTCGTCCACCTCGATCCACAGCTCTGC
 CTGACTCCACTGAAGCAAACACACATCACTGAGGTACAGCCTCTGCCAGACCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTCACCTCATGCCACGGTGGGACCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGCAGACGCCGGGCCAGGCCATGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCCTGGAAAGAAACCTCAGCCCTCTGTGAGACACCAAGTTACGTC
 AAAGTCAGGAGCAGCTCCGCTCCATAGAGGCTGGTCAGCAGTGGCAAACAAACTTC
 CTTTGTGGGAGCTCTGCTTCCCTACAGCCCTCGGAAGCGCCCTCAAGAACCTCACCC
 CTTCAAGAGACCCGACCATGGACATCGCAACCAAGGGCCCTCCCCACCAGCAGGGACCC
 CTTCCCTCTGTCCCTCGACTACAACCAACAGCAGCCAGGGAGCAACAGCACCTAGCCAA
 GATCACAACTCAGCGAAGACCAAGCATGAGGCCAACAGCCACGCCAGACTGCCGGAC
 GAGGCCGACACAGAC**TGA**GTGAGGTGAAATGGGTTCTCCCTCGGGCTGAGTG
 TGGCTCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAAGCAGCTCAC
 CGGGAACTCCACGCCACGCGCTCACTCCAGGTCTCTTACTGCGTGTCAAGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCGGTATGCCAAAGAGGGTGTGCCCTAGCCTG
 GGCCCCCAGGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCACGCCCTAACCCAGATGTGGCAACAGGACCCCTGCTCACATCAC
 CGGACTGTATGTATGGGAGGGCTCACCTGTTCCAGAGGTGTCTGGACTCACCTGG
 CACATGTTCTGTGTTCAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
 TTAAAAATTCACTCAGTGTGGCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCEVGVGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLSE
ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSPNFMVLIATSVETSAAGSPEGAGM
TTVQTITGSDPEEAIFDTLCTDDSSEEAKTLTMDILTLAHTSTEAKGLSSESSASSDGPHPV
ITPSRASESSASSDGPVITPSRASESSASSDGPVITPSWSPGSVDVTLLAEALVTVTNI
EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTSDDPPALPDSTEAKPHITEVTVASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPEGATTLSGALVTVSRNPLEETSALSVETPSY
VKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEAAALKNFTPSETPTMDIATKGPFPQRSTD
PLPSVPPTTNSSRGNTNLAKITTSAKTTMKGPKQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GGGGAGCATCGCTGCGGTCTCGCGAGACCCCGGCCGATTGCCGCTCTCCCGGG
GGCGCAGACGAGCTTCGCTCGCAGCTGGATGCCAGCAGGGGCCGCGGGTCTCGAGCCCA
GAGAGAAATCTCATCTGCGAGCTTAAAGCAAATAAGCACAGAGGGAGATTAT
CCTTGACCTTTGAAGACAAAAGTAAACTGAAATTAAA**ATG**TCTCGGGGAGAAGGGAG
CTTGACTTACACTTGTGATAATATGCTCTGCACATAGGCTGTGCTAGTCAGAAATT
GCCTCAGAACAGACTTGAAGATGTGCTATTGACATCAGCATTCTCTTAAGGAAATC
AGAGGAATGAGCCCGTATATACCTCAACTAAGAGACTGCATTAAATTCTGCTGTCAAC
AAAAAAACATATCAGGGGACAAAGCATGTAACCTGTGATCTCGACACTCGAAAACAGCTA
GACAACCCAACTGCTACCTATTTCTGCCCCAACAGGAGAACGGCTGTCATTGAAACAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTCTTCCATCTTGACCAGAATTGCGAAG
CCAAGAGTTACCCCAGGAAGATTCTCTTACATGGCAATTTCACAAGCAGTCACCCCC
TAGGCCATCATCACACAGATTCAAAGGCCACCGATATCTAGGAGAGACCCACTTCT
CAAGAGTTGGATCTCATGATCACCTGGAGAACATTAACTAGGATGAGAACAGTGCCCA
GCTCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCAAAATTCTCTGATCAAGAAA
TAGCTCATCTGCTGCTGAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTCTCTCCA
CATACCACTCGGGTACTCAGGCCAACAGGCCACCCCTTACCCACCAATGCTCAGGACCC
TTCTGGACTTCCCAGGCCACAGTGGCCACACAGCTCCACCTGTAACCCACTGTCACCTCT
AGCCTCCACGACCTCATTCAGTTTACACGGCTGGGCTACACTCCAAGGAATG
GCTAACACAGCAGTCTGACTAACCTTCAGGCCACTACGGACTCAGGAGCTAG
AACCATACGGTTTACAGAAATCTCCTAACTTGAACACAGGGAAATGTGATAACCTTA
CTGCACTTTCTATGCAATGTGGAGTCTTCACTATGAATAAAACTGCTCTGGAAAGGT
AGGGAGGCCAGTCAGGCCAGTCTCCAGGGCTAGTGTCCAGAAAATCAGTAGGCCCTTC
ATTGGAAAATAGCTCTTATCGGCTCTCTCTGGTGTCTGGTGTCTGGTGTAGGCC
CTGCTCTCTGGTGTAGAATCTTCGGAACTACTCGCAGGAAACGTTACTCAAGACTGGAT
TATTGATCAATGGGATCTAGTGGACAT**TAAG**GATGGAACTCGGTGCTCTTAATTCTT
TAGTAACCAAGAGGAAAATGCAATGAGTTCTGCTGACTGTGAGTTCTAGCAGGGAGTTG
TATTGIAAGACAGGAAAATGGCCCTTCTGCTTCTTCTTCTGGAGACAGACTCTT
GCTCTGTGCCAGGCTGGAGTCAGTACAGGCCACTCGCTCTCACGCCAACCTCCGCTC
CTGGGTCAGGCCAGGATTCTCGCTCAGGCTTCAAGTATCTGGGATACAGGCTGTGCCA
CCACACTGGGTGATTCTTGTATTGTTAGAGACGGGTTTCCAGATTGCTCAGGGT
GTCTCAAACCTCTGACCTAGTGTACCTACCCCTCTCGGCCCTCCAAAGTGTGGGATTACAGG
CATGACCCACACAGCTGGCCCTTCTGTTTATGTTGGGTTTGTGAGAAGGAATGAGT
GGAAACCAAAATTAGTGAATTGGGAACTATGCTCTAAAAATTAGTGAACAAACAGCTCT
ATGTAAGTAATAAAAGTATAATTGCCATATAATTCAAAATTCAACTGGCTTATGCCAA
GAAACAGGTAGGACATCTAGGTTCCAATCATTACACATTCTGGTTCAGATAAAATCAAC
TGTATATCAATTCTAATGGATTGCTTTCTTTTATGATGGATTCTTAAAACCTTATT
CCAGATGAGTCTCTTCAATTATTGTAATAACATTGTTACTCTAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTRLASQNLKKSLEDVVIDIQSSLKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLPKAAGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFQGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTVTSPPTTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLLETIPFTEISNLNTLNGNVYNPTALSMSNVESSTMNKTAWEGRREASPGSSSQGSV
PENQYGLPFEKWLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

T2526650

FIGURE 329

CTCCCACGGTGTCCAGCGCCCAGA **ATG** CGGCTTCTGGTCCTGCTATGGGTTGCCGTGCTGCT
 CCCAGGTATGAAGCCTGAGGGCCCCAGAGGAAATCACGGGTTGCAAGGGGACACTGTGTT
 CCCTGCAGTGCACCTACAGGGAAAGAGCTGAGGGACACCAGGAAGTACTGGTGCAGGAAGGGT
 GGATCCTCTCTCTCGCTGCTCTGGCACCATCTAGCAGAAAGAAGGGCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCGCCAGAGCTCTGCCTCATTTGTGACCCCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGTGAAAACAGGGGCCCGATGAG
 TCTTACTGATCTCTGTCGTCCTCCAGGACCTGCTGTCCTCCCTCCCTCTCCAC
 CTTCCAGCCTCTGGCTAACACAGCCTGAGCAGGCAAGGAAAGCTCAGCAAACCCAGC
 CAGGATTGACTTCTCTGGCTTACCCGGCAGGCCAACAGCAGGAGGGAAAGACAGGG
 GCTGAGGCCCTCATGGCAGGGACTTCCCAGTACGGGACGGAAAGGACTTCTCAGTACAC
 AGGAACACTCTCCTCACCCAGGACCTCTCCCTCGAGGGAGCTCCCGGCCCTCCATGAGC
 TGGACTCCACCTCAGCAGAGGACACCAGCTCAGCTCAGTGGCAGCTAAGGCCAG
 GTGTCATCCCGATGGTCCGATCTGGCCCATACTGGCCCGACTCTGGTGCTGCTGAGCCTTCTGT
 CGCAGGCTGATGCCCTCTGGCAGGCCACCTGCTCTGGAGAAGGAAGCTCAACAGGCC
 CGGAGACACAGAGGAACGAGAAAGTCTGGTCTCAGCTGACTGCGGAGGAAAGAG
 CCTTCCAGGCCCTGAGGGGAGCTGATCTGATGCCCTCCACACATCTGAGGAGGA
 GCTGGCTTCTGAGTTGTCAGCG **TAG** GCGAGGAGGCCCTGTGCCAGGCCAGCAGT
 GAAGGACTATGGCTGGTGATGCCACGGCAGATTCCCGGAAAGCTTCCACCTGCCTCAGAG
 TCCAGCTGCCGACTCCAGGGCTCTCCCCACCTCCCGAGGCTCTCTGTGATGTTCCA
 GCCTGACCTAGAACGCTTGTGAGCCCTGAGGCCAGAGCGGTTGCTGCTCTCCGGCTG
 GAGACTGGGACATCCGTAGTGGTTCACATCCCTGGCAGACTACAGGCCAGTGC
 GCAGGGCCAGAACAGGGCTAGGGATCTGAGTTCAATCTGCCAGGAACCTCTGGC
 CTCTAGGCCAGTGTGGACCCCTGCCCTCCACTCCAGACCCCCACCTGTCTCCCTCCC
 TGGCCTCAGACTTAGTCCACGGTCTCTGATCAGCTGAGTGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATCTGGCTTCTTGTGAAGGACCTCTGGCATCAGGCCCTTCAAGGC
 GTGAAAAACGTGATTCTGGGCCACCAAGACCCACAAAACCATCTCTGGCTTGTGAG
 GACTCTGAGTCTAACATGCCAGTGACTGTCGACTTGAAGTTGAGGGCAGTGGGCTG
 ATGAACGCTCACACCCCTCAGCTTAGAGTCTGCAATTGGGCTGACGCTTCACTCC
 CAATAGATCTGCTCTGAGCTGGACACAGATGCCACAGTGGGACTCCCCCTGAGGCC
 TCAAGGCCCTGGTCAAGGTGCAATTGCAAGGATAAGCCAGGCCACAGAACAGTGG
 TTGCTTNCATTTGCCCTCCCTGGNCATGCCCTCTGGCTTGGAAAAAAATGTAAGA
 AAACCTTGCCCTCTTGTGAGGGTACTGCCTATGGGTTCTGGGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGACGTGAGGTGCTAACACAGAGGAGACTAGGA
 CAGGCCGGATACCTGAGGTGACTCCGAGTCCAGGCCCTGGAGAAGGGTGGGGT
 GCACAACTACTATTTTTCTTCCATTATTAGTTAGGTTAAAGACAGAAATCTGCTG
 GCTGCCAGGTGGAGTGCAAGTGGCACGATCTGCAAAACTCCGCCCTGGGTCAAGT
 GATTCTCTGCCCTAGCCTCCGAGTAGCTGGGATTACAGGCCAGCACACCAC
 CTGGCTAATTGTTGACTTTAGTAGAGATGGGGTTACCATGTTGCCAGGCTG
 GCTGAGCTCCCTGCTCAGTCCTCCAAATTGCCGGGATTACAGGCCATG
 GACCTGCAAAATCTGGAAAGTCTGAGTGTGCAAGTGCACCCATAGTCT
 ACCAGAGGACTATCATTTGCTTCTCCACTTCTCTTCACATAATTG
 CGGGTGTCTTCAACTTGTGATATACAACCTTGATCTGCCCTTCA
 CCTTACAGAGCAATTATCTGATATACAACCTTGATCTGCCCTTCA
 CCTTACATTTATCCAGCAGCTCTGTTACAGACCTTTATAA
 AATGTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196
<subunit 1 of 1, 332 aa, 1 stop
<MW: 36143, pI: 5.89, NX(S/T): 1
MRLLVLLWGCLLPGYEALEGPEEISGFEGDTVSLQCTYREELDHRKYWCRKGGILFSRCS
GTIYAAEEGQETMKGRVSIRDQRQELSLIVTLWNLTLDAGEYWCGVEKRGPDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAQQTQPPGLTPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSaedTSPALSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLRSRLTAEEKEAPSQAPEGD
VISMPPLHTSEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128